



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 184522

TO: Celine Qian
Location: REM/2A64/2C70
Art Unit: 1636
Tuesday, April 11, 2006
Case Serial Number: 10/696708

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Qian,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

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ACCESS DB # 184522
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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 4/6/06
Art Unit: 1636 Phone Number: 2-0777 Serial Number: 101696708
Location (Bldg/Room#): 2A64 (Mailbox #): 2C70 Results Format Preferred (circle): TAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Mutations in and Genomic structure of HERG

Inventors (please provide full names): _____

Earliest Priority Date: 7/27/1998

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 60 and 61.

60 Na 20

61 Na 20

mg

*WHL
4/11*

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GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: April 10, 2006, 15:06:53 ; Search time 311.5 Seconds
(without alignments)
256.858 Million cell updates/sec

Title: US-10-696-708A-61

Perfect score: 20

Sequence: 1 ttgacccgcgcctgctcgt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues 18535810

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*
1: /SID55/ptcodata/2/pubpna/US06_NEW_PUB.seq:*
2: /SID55/ptcodata/2/pubpna/US06_NEW_PUB.seq:*
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5: /SID55/ptcodata/2/pubpna/US05_NEW_PUB.seq:*
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13: /SID55/ptcodata/2/pubpna/US11_NEW_PUB.seq4:*
14: /SID55/ptcodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SID55/ptcodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	82.0	639	US-09-925-065A-413820	Sequence 413820,
2	16.4	82.0	644	US-10-301-480-479809	Sequence 479809,
3	16.4	82.0	644	US-10-301-480-1093218	Sequence 1093218,
4	15.8	79.0	503	US-09-925-065A-24467	Sequence 24467, A
5	15.8	79.0	503	US-10-301-480-125704	Sequence 125704,
6	15.8	79.0	503	US-10-301-480-739113	Sequence 739113,
7	15.8	79.0	3431	US-11-245-147-174	Sequence 174, App
8	15.4	77.0	566	US-09-925-065A-473258	Sequence 473258,
9	15.4	77.0	566	US-09-925-065A-473259	Sequence 473259,
10	15.4	77.0	988	US-10-301-480-586930	Sequence 586930,
11	15.4	77.0	988	US-10-301-480-1200339	Sequence 1200339,
12	15.4	77.0	1080	US-11-055-822-333	Sequence 333, App
13	15.4	77.0	1296	US-11-055-822-59	Sequence 59, App
14	15.4	77.0	1296	US-11-055-822-327	Sequence 327, App
15	15.4	77.0	1296	US-11-055-822-327	Sequence 327, App
16	15.4	77.0	2337	US-11-072-512-160	Sequence 160, App
17	15.4	77.0	2422	US-11-072-512-1133	Sequence 1133, App
18	15.4	77.0	2467	US-11-080-991-107	Sequence 107, App

19	15.4	77.0	2479	US-10-955-054A-50	Sequence 50, App
20	15.4	77.0	2921	US-10-750-185-34096	Sequence 34096, A
21	15.4	77.0	2921	US-10-750-623-34096	Sequence 26, App
22	15.4	77.0	63984	US-11-121-086-26	Sequence 1690, App
23	15.4	77.0	1694969	US-10-506-454-1690	Sequence 303211,
24	15.2	76.0	25	US-11-136-527-303211	Sequence 80702, A
25	15.2	76.0	201	US-10-995-561-80702	Sequence 423156,
26	15.2	76.0	549	US-09-925-065A-423156	Sequence 487510,
27	15.2	76.0	552	US-10-301-480-487510	Sequence 1100919,
28	15.2	76.0	552	US-10-301-480-1100919	Sequence 41469, A
29	15.2	76.0	563	US-10-301-480-41469	Sequence 654878,
30	15.2	76.0	563	US-10-301-480-654878	Sequence 451154,
31	15.2	76.0	621	US-09-925-065A-51154	Sequence 510257,
32	15.2	76.0	635	US-10-301-480-510257	Sequence 1123666,
33	15.2	76.0	635	US-10-301-480-1123666	Sequence 123, App
34	15.2	76.0	717	US-10-714-887-123	Sequence 6416, App
35	15.2	76.0	1400	US-11-136-527-6416	Sequence 814, App
36	15.2	76.0	1541	US-10-909-125-814	Sequence 727546,
37	15.2	76.0	1558	US-09-925-065A-727546	Sequence 2320, App
38	15.2	76.0	1861	US-11-136-527-2320	Sequence 1, App
39	15.2	76.0	33014	US-11-077-716-1	Sequence 1, App
40	15.2	76.0	33592	US-11-249-873-1	Sequence 3, App
41	15.2	76.0	33699	US-11-249-873-3	Sequence 14, App
42	15.2	76.0	33988	US-11-249-873-14	Sequence 2, App
43	15.2	76.0	34341	US-11-249-873-2	Sequence 4, App
44	15.2	76.0	34448	US-11-249-873-4	Sequence 479, App
45	15.2	76.0	34555	US-10-623-155-479	

ALIGNMENTS

RESULT 1
US-09-925-065A-413820/C
Sequence 413820, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 413820
LENGTH: 639
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-413820

Query Match
Best Local Similarity 82.0% Score 16.4; DB 6; Length 639;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
DB 155 TTGACCCGCCCCCTGTC 148
QY 1 TTGACCCGCCCCCTGTC 18
US-10-301-480-479809/C
Sequence 479809, Application US/10301480

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Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 479809
LENGTH: 644
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-479809

Query Match      82.0%; Score 16.4; DB 10; Length 644;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGACCCCGCCCTGTGTC 18
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Db      165 TTGACCCCACTGCTGTC 148

RESULT 3
US-10-301-480-1093218/c
Sequence 1093218, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1093218
LENGTH: 644
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-1093218

Query Match      82.0%; Score 16.4; DB 10; Length 644;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGACCCCGCCCTGTGTC 18
      |||||
Db      165 TTGACCCCACTGCTGTC 148

RESULT 4
US-09-925-065A-24467/c
Sequence 24467, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24467
LENGTH: 503
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-24467

Query Match      79.0%; Score 15.8; DB 6; Length 503;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGACCCCGCCCTGTGTC 19
      |||||
Db      241 TTGACCTGCTGCTGTC 223

RESULT 5
US-10-301-480-125704/c
Sequence 125704, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 125704
LENGTH: 503
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-125704

Query Match      79.0%; Score 15.8; DB 9; Length 503;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGACCCCGCCCTGTGTC 19
      |||||
Db      241 TTGACCTGCTGCTGTC 223

RESULT 6
US-10-301-480-739113/c
Sequence 739113, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
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; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 739113
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-739113

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Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGTCG 19
|||
Db 241 TTGACCTGTGCTGTCG 223

RESULT 7
US-11-245-147-174/c
; Sequence 174, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:

APPLICANT: GARCIA, TERESA
APPLICANT: ROMAN ROMAN, SERGIO
APPLICANT: BARON, ROLAND
APPLICANT: CALL, KATHERINE
APPLICANT: THEILHABER, JOACHIM
APPLICANT: CONNOLLY, TIMOTHY
APPLICANT: JACKSON, AMANDA
APPLICANT: BUSHNELL, STEVEN
APPLICANT: RAMADI, GEORGES
TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
FILE REFERENCE: 37991-0023
CURRENT APPLICATION NUMBER: US/11/245,147
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,400
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 246
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 174
LENGTH: 3431
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Homo sapiens elastin microfibril interface located
US-11-245-147-174

Query Match 79.0%; Score 15.8; DB 11; Length 3431;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGTGTCG 20
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Db 779 TGACCCAGCTCTGTGTCG 761

RESULT 8
US-09-925-065A-473258
; Sequence 473258, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 473258
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-473258

Query Match 77.0%; Score 15.4; DB 6; Length 566;
Best Local Similarity 94.1%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGTGTC 18
|||
Db 299 TGACCCCGCCCTGTGTC 315

RESULT 9
US-09-925-065A-473259
; Sequence 473259, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 473259
LENGTH: 566
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-473259

Query Match 77.0%; Score 15.4; DB 6; Length 566;
Best Local Similarity 94.1%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGTGTC 18
|||
Db 299 TGACCCCGCCCTGTGTC 315

RESULT 10
US-10-301-480-586930
; Sequence 586930, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21

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; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 586930
; LENGTH: 988
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-586930

Query Match          77.0%; Score 15.4; DB 10; Length 988;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TTGACCCGCGCCCTGT 17
        |||||
Db      909 TTGACCCGCGCCCTGT 925

RESULT 11
US-10-301-480-1200339
; Sequence 1200339, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1200339
; LENGTH: 988
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1200339

Query Match          77.0%; Score 15.4; DB 10; Length 988;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TTGACCCGCGCCCTGT 17
        |||||
Db      909 TTGACCCGCGCCCTGT 925

RESULT 12
US-11-055-822-333
; Sequence 333, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
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; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 333
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1057)
; OTHER INFORMATION: RXA02158
US-11-055-822-333

Query Match          77.0%; Score 15.4; DB 14; Length 1080;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TTGACCCGCGCCCTGT 17
        |||||
Db      13 TTGACCCGCGCCCTGT 29

RESULT 13
US-11-055-822-59
; Sequence 59, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
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; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
```



```
SEQ ID NO 59
LENGTH: 1296
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1273)
OTHER INFORMATION: RKS02157
US-11-055-822-59
```

```
Query Match          77.0%; Score 15.4; DB 14; Length 1296;
Best Local Similarity 94.1%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 TTGACCCGCGCCCTGCT 17
         |||||
Db      1202 TTGACCCGCGCCCTGCT 1218
```

```
RESULT 14
US-11-055-822-299
Sequence 299, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroeder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberbauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BGI-121CPN
CURRENT FILING DATE: 2005-02-11
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 299
LENGTH: 1296
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1273)
OTHER INFORMATION: RKS02157
US-11-055-822-299
```

```
Query Match          77.0%; Score 15.4; DB 14; Length 1296;
Best Local Similarity 94.1%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 TTGACCCGCGCCCTGCT 17
         |||||
Db      1202 TTGACCCGCGCCCTGCT 1218
```

```
RESULT 15
US-11-055-822-327
Sequence 327, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroeder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberbauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BGI-121CPN
CURRENT FILING DATE: 2005-02-11
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 327
LENGTH: 1296
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1273)
OTHER INFORMATION: RKA02157
US-11-055-822-327
```

```
Query Match          77.0%; Score 15.4; DB 14; Length 1296;
Best Local Similarity 94.1%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TTGACCCGCGCCCTGCT 17
         |||||
Db      1202 TTGACCCGCGCCCTGCT 1218
```

Search completed: April 10, 2006, 15:25:08
Job time : 313.5 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: April 10, 2006, 15:06:00 ; Search time 442 Seconds
(without alignments)
374.180 Million cell updates/sec

Title: US-10-696-708A-61
Perfect score: 20
Sequence: 1 ttgaccccgccctgctgct 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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3: /cgn2_6/ptodata/1/pubphna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubphna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubphna/US10A_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubphna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubphna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-735-995-61
2	20	100.0	20	7	US-10-696-708-61
3	18.4	92.0	477	5	US-10-027-632-14963
4	18.4	92.0	477	6	US-10-027-632-14963
5	17.4	87.0	897	6	US-10-156-761-5165
6	17.4	87.0	9025608	6	US-10-156-761-1
7	16.8	84.0	303	8	US-10-425-115-97440
8	16.8	84.0	1017	7	US-10-282-112A-7484
9	16.4	82.0	279	8	US-10-423-115-61568
10	16.4	82.0	639	4	US-09-925-065A-413820
11	16.4	82.0	826	4	US-10-425-115-152918
12	16.4	82.0	890	7	US-10-425-114-34159
13	16.4	82.0	1124	7	US-10-425-114-24374
14	16.4	82.0	1483	7	US-10-425-114-21303
15	16.4	82.0	1644	6	US-10-156-761-4733
16	16.4	82.0	1672	6	US-10-425-115-152919
17	15.8	79.0	252	7	US-10-437-963-76954
18	15.8	79.0	317	8	US-10-425-115-147751
19	15.8	79.0	432	8	US-10-425-115-108758
20	15.8	79.0	473	7	US-10-437-963-73996
21	15.8	79.0	503	4	US-09-925-065A-24467
22	15.8	79.0	568	7	US-10-767-701-965
23	15.8	79.0	865	8	US-10-425-115-6921

24	15.8	79.0	1008	3	US-09-815-242-8010	Sequence 8010, Ap
25	15.8	79.0	1788	7	US-10-437-963-5286	Sequence 5286, Ap
26	15.8	79.0	1842	7	US-10-437-963-10345	Sequence 10345, A
27	15.8	79.0	2093	8	US-10-930-301-106	Sequence 106, Ap
28	15.8	79.0	2763	6	US-10-236-055A-25	Sequence 25, Appl
29	15.8	79.0	2803	8	US-10-723-860-5136	Sequence 5136, Ap
30	15.8	79.0	3431	8	US-10-473-974-174	Sequence 174, Appl
31	15.8	79.0	3667	9	US-10-852-335A-70	Sequence 70, Appl
32	15.8	79.0	5846	3	US-09-764-877-3119	Sequence 3119, Ap
33	15.8	79.0	5846	6	US-10-242-515-3319	Sequence 3319, Ap
34	15.8	79.0	5848	3	US-09-764-877-3320	Sequence 3320, Ap
35	15.8	79.0	5848	6	US-10-242-515-3320	Sequence 3320, Ap
36	15.8	79.0	28614	5	US-10-087-152-1027	Sequence 1027, Ap
37	15.8	79.0	39768	5	US-10-087-152-1030	Sequence 1030, Ap
38	15.8	79.0	72732	7	US-10-052-482-193	Sequence 193, Ap
39	15.4	77.0	147	3	US-09-867-701-2738	Sequence 2738, Ap
40	15.4	77.0	269	7	US-10-424-599-105108	Sequence 105108, Ap
41	15.4	77.0	339	7	US-10-437-963-91494	Sequence 91494, A
42	15.4	77.0	366	8	US-10-425-115-24864	Sequence 24864, A
43	15.4	77.0	448	7	US-10-424-599-77596	Sequence 77596, A
44	15.4	77.0	566	4	US-09-925-065A-473258	Sequence 473258, A
45	15.4	77.0	566	4	US-09-925-065A-473259	Sequence 473259, A

ALIGNMENTS

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RESULT 1
US-09-735-995-61
; Sequence 61, Application US/09735995
; Patent No. US20010034024A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/735,995
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/226,012
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-995-61

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      TTGACCCCGCCCTGCTGCT 20
Db      1      TTGACCCCGCCCTGCTGCT 20

RESULT 2
US-10-696-708-61
; Sequence 61, Application US/10696708
; Publication No. US20040078833A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; FILE REFERENCE: 2323-164
; CURRENT APPLICATION NUMBER: US/10/696,708
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 09/735,995
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US 09/226,012
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; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 09/122,847
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-696-708-61
```

```
Query Match          100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 TTGACCCCGCCCTGTGCT 20
    |||||
Db 1 TTGACCCCGCCCTGTGCT 20
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RESULT 3

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US-10-027-632-14963/c.
; Sequence 14963, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14963
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-14963
```

```
Query Match          92.0%; Score 18.4; DB 5; Length 477;
Best Local Similarity 95.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 TTGACCCCGCCCTGTGCT 20
    |||||
Db 429 TTGACACCGCCCTGTGCT 410
```

RESULT 4

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US-10-027-632-14963/c
; Sequence 14963, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
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```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14963
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-14963
```

```
Query Match          92.0%; Score 18.4; DB 6; Length 477;
Best Local Similarity 95.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 TTGACCCCGCCCTGTGCT 20
    |||||
Db 429 TTGACACCGCCCTGTGCT 410
```

RESULT 5

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US-10-156-761-5165
; Sequence 5165, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5165
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(897)
US-10-156-761-5165
```

```
Query Match          87.0%; Score 17.4; DB 6; Length 897;
Best Local Similarity 94.7%; Pred. No. 99;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 TTGACCCCGCCCTGTGCTG 19
    |||||
Db 808 TTCACCCCGCCCTGTGCTG 826
```

RESULT 6

```
US-10-156-761-1
; Sequence 1, Application US/10156761
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```
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

```
Query Match      87.0%; Score 17.4; DB 6; Length 9025608;
Best Local Similarity 94.7%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TTGACCCCGCCCTGTGCTG 19
DB      6288491 TTGACCCCGCCCTGTGCTG 6288509
```

```
RESULT 7
US-10-425-115-97440
; Sequence 97440, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 97440
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_2037C.1
US-10-425-115-97440
```

```
Query Match      84.0%; Score 16.8; DB 8; Length 303;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 TTGACCCCGCCCTGTGCTG 20
DB      56 TTGACCTCGCCCGCCGTCGT 75
```

```
RESULT 8
US-10-282-122A-7484/C
; Sequence 7484, Application US/10282122A
; Publication No. US20040029129A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7484
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-7484
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Query Match      84.0%; Score 16.8; DB 7; Length 1017;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 TTGACCCCGCCCTGTGCTG 20
DB      608 TTGACCCCGCCCATGTGCTG 589
```

```
RESULT 9
US-10-425-115-61568/C
; Sequence 61568, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 61568
; LENGTH: 279
; TYPE: DNA
```

```

; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_156144C.1
US-10-425-115-61568

Query Match          82.0%; Score 16.4; DB 8; Length 279;
Best Local Similarity 94.4%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 TGACCCCGCCCTGTGTC 19
Db      50 TGATCCCGCCCTGTGTC 33

RESULT 10
US-09-925-065A-413820/c
; Sequence 413820, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413820
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-413820

Query Match          82.0%; Score 16.4; DB 4; Length 639;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 TTGACCCCGCCCTGTGTC 18
Db      165 TTGACCCCGCCCTGTGTC 148

RESULT 11
US-10-425-115-152918
; Sequence 152918, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 152918
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: (1)..(826)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71044C.1
US-10-425-115-152918

Query Match          82.0%; Score 16.4; DB 8; Length 826;
Best Local Similarity 94.4%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 TGACCCCGCCCTGTGTC 19
Db      518 TGACCCCGCTCTGTGTC 535

RESULT 12
US-10-425-114-34159
; Sequence 34159, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 34159
; LENGTH: 890
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO1723B10_FLI
US-10-425-114-34159

Query Match          82.0%; Score 16.4; DB 7; Length 890;
Best Local Similarity 94.4%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 TGACCCCGCCCTGTGTC 19
Db      36 TGACCCCGCTCTGTGTC 53

RESULT 13
US-10-425-114-24374
; Sequence 24374, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24374
; LENGTH: 1124
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3608-041-A7_FLI
US-10-425-114-24374
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Query Match 82.0%; Score 16.4; DB 7; Length 1124;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGGTCG 19
|||||
Db 55 TGACCCCGCTCCTGGTCG 72

RESULT 14

US-10-425-114-21303
; Sequence 21303, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21303
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-223-Cl1_FLI
US-10-425-114-21303

Query Match 82.0%; Score 16.4; DB 7; Length 1483;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGGTCG 19
|||||
Db 574 TGACCCCGCTCCTGGTCG 591

RESULT 15

US-10-156-761-4733
; Sequence 4733, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4733
; LENGTH: 1644
; TYPE: DNA

; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1644)
US-10-156-761-4733

Query Match 82.0%; Score 16.4; DB 6; Length 1644;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGGTCG 19
|||||
Db 65 TGACCCCGCACCTGGTCG 82

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Job time : 454 sec

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OM nucleic - nucleic search, using SW model

Run on: April 10, 2006, 15:02:55 ; Search time 76 Seconds
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Title: US-10-696-708A-61
Perfect score: 20
Sequence: 1 ttgaccccgccctgctcgt 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-226-012-61 Sequence 61, Appl
2	16.8	84.0	1026	3	US-09-252-991A-3069 Sequence 3069, Ap
3	16.8	84.0	1053	3	US-09-252-991A-2966 Sequence 2966, Ap
4	16.8	84.0	1617	3	US-09-252-991A-2905 Sequence 2905, Ap
5	15.8	79.0	501	3	US-09-252-991A-3301 Sequence 3301, Ap
6	15.8	79.0	735	3	US-09-134-001C-25 Sequence 25, Appl
7	15.8	79.0	819	3	US-09-134-001C-27 Sequence 27, Appl
8	15.8	79.0	1020	3	US-09-252-991A-2226 Sequence 2226, Ap
9	15.8	79.0	1038	3	US-09-252-991A-2301 Sequence 2301, Ap
10	15.8	79.0	1221	3	US-09-252-991A-2611 Sequence 2611, Ap
11	15.8	79.0	1965	3	US-09-252-991A-3234 Sequence 3234, Ap
12	15.8	79.0	2093	3	US-09-398-522-106 Sequence 106, App
13	15.8	79.0	2325	3	US-09-252-991A-3413 Sequence 3413, A
14	15.8	79.0	70308	3	US-09-949-016-15601 Sequence 15601, A
15	15.4	77.0	2337	3	US-10-104-047-160 Sequence 160, App
16	15.4	77.0	2418	3	US-09-949-016-1694 Sequence 1694, Ap
17	15.4	77.0	2422	3	US-10-104-047-1133 Sequence 1133, Ap
18	15.4	77.0	3243	2	US-08-239-276-6 Sequence 6, Appl
19	15.4	77.0	3243	2	US-08-468-579B-6 Sequence 6, Appl
20	15.4	77.0	3243	3	US-08-468-577B-6 Sequence 6, Appl
21	15.4	77.0	3243	3	US-08-468-581A-6 Sequence 6, Appl
22	15.4	77.0	3478	3	US-09-949-016-55257 Sequence 5257, Ap
23	15.4	77.0	3493	3	US-09-949-016-780 Sequence 780, App
24	15.4	77.0	16365	3	US-09-949-016-13436 Sequence 13436, A

25	15.4	77.0	19009	3	US-09-949-016-12522	Sequence 12522, A
26	15.4	77.0	19012	3	US-09-949-016-16999	Sequence 16999, A
27	15.4	77.0	29614	3	US-09-949-016-12390	Sequence 12390, A
28	15.4	77.0	30922	3	US-09-949-016-16700	Sequence 16700, A
29	15.2	76.0	354	3	US-09-621-976-19114	Sequence 19114, A
30	15.2	76.0	500	3	US-09-370-838-142	Sequence 142, App
31	15.2	76.0	500	3	US-09-854-133-142	Sequence 142, App
32	15.2	76.0	601	3	US-09-949-016-29433	Sequence 29433, A
33	15.2	76.0	601	3	US-09-949-016-184859	Sequence 184859, A
34	15.2	76.0	601	3	US-09-949-016-184859	Sequence 184859, A
35	15.2	76.0	601	3	US-09-949-016-185013	Sequence 185013, A
36	15.2	76.0	601	3	US-09-949-016-185014	Sequence 185014, A
37	15.2	76.0	601	3	US-09-949-016-191015	Sequence 191015, A
38	15.2	76.0	1173	3	US-09-543-681A-2243	Sequence 2243, Ap
39	15.2	76.0	1522	3	US-09-949-016-5464	Sequence 5464, Ap
40	15.2	76.0	1541	3	US-09-949-016-590	Sequence 590, App
41	15.2	76.0	1843	3	US-09-780-045-10	Sequence 10, Appl
42	15.2	76.0	2574	3	US-09-780-045-3	Sequence 3, Appl
43	15.2	76.0	18008	3	US-09-949-016-12391	Sequence 13291, A
44	15.2	76.0	30773	3	US-09-949-016-12332	Sequence 12332, A
45	15.2	76.0	30773	3	US-09-949-016-17206	Sequence 17206, A

ALIGNMENTS

RESULT 1
US-09-226-012-61
Sequence 61, Application US/09226012
Patent No. 6207383
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226.012
CURRENT FILING DATE: 1999-01-06
EARLIER APPLICATION NUMBER: 09/122,847
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-226-012-61

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGCTGCT 20
DB 1 TTGACCCCGCCCTGCTGCT 20

RESULT 2
US-09-252-991A-3069/C
Sequence 3069, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.116
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 3069
LENGTH: 1026
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3069

Query Match 84.0%; Score 16.8; DB 3; Length 1026;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCT 20
Db 617 TTGACCCCGCCCATGTGCT 598

RESULT 3
US-09-252-991A-2966/C
Sequence 2966, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2966
LENGTH: 1053
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2966

Query Match 84.0%; Score 16.8; DB 3; Length 1053;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCT 20
Db 600 TTGACCCCGCCCATGTGCT 581

RESULT 4
US-09-252-991A-2905
Sequence 2905, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2905
LENGTH: 1617
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2905

Query Match 84.0%; Score 16.8; DB 3; Length 1617;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCT 20

Db 653 TTGACCCCGCCCATGTGCT 672

RESULT 5
US-09-252-991A-3301
Sequence 3301, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3301
LENGTH: 501
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3301

Query Match 79.0%; Score 15.8; DB 3; Length 501;
Best Local Similarity 89.5%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGACCCCGCCCTGTGCT 20
Db 305 TGACCCCGCCCATGTGCT 323

RESULT 6
US-09-134-001C-25
Sequence 25, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: US/09/134,001C
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 25
LENGTH: 735
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-25

Query Match 79.0%; Score 15.8; DB 3; Length 735;
Best Local Similarity 89.5%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCT 19
Db 221 TTGACCCCGCCCTGTGCT 239

RESULT 7
US-09-134-001C-27/C
Sequence 27, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS


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RESULT 12
US-09-398-522-106/c
; Sequence 106, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (0)...(0)
; OTHER INFORMATION: CACNAIG Cpg ISLAND
US-09-398-522-106

Query Match          79.0%; Score 15.8; DB 3; Length 2093;
Best Local Similarity 89.5%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGACCCCGCCCTGTGCTGT 20
DB      1380 TGACCCCGCCCTGTGCTGT 1362

RESULT 13
US-09-252-991A-3413/c
; Sequence 3413, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3413
; LENGTH: 2325
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3413

Query Match          79.0%; Score 15.8; DB 3; Length 2325;
Best Local Similarity 89.5%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGACCCCGCCCTGTGCTGT 20
DB      193 TGACCCCGCCCTGTGCTGT 175

RESULT 14
US-09-949-016-15601/c
; Sequence 15601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15601

Query Match          79.0%; Score 15.8; DB 3; Length 70308;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGACCCCGCCCTGTGCTGT 20
DB      2650 TGACCCCGCCCTGTGCTGT 2632

RESULT 15
US-10-104-047-160/c
; Sequence 160, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-160

Query Match          77.0%; Score 15.4; DB 3; Length 2337;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGACCCCGCCCTGTGT 17
DB      1599 TTGACCCCGCCCTGTGT 1583
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Search completed: April 10, 2006, 15:05:37
Job time : 77 secs

ORIGIN Jovv-en-Josias cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

Query Match 90.0%; Score 18; DB 5; Length 780;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGTC 18
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Db 590 TTGACCCCGCCCTGTGTC 607

RESULT 2
BG961818 860 bp mRNA linear EST 12-JUN-2001
LOCUS 602826471P1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4981433 5',
DEFINITION mRNA sequence.
ACCESSION BG961818
VERSION BG961818.1 GI:14349455
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 860)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10982 row: m column: 18
High quality sequence stop: 456.
Location/Qualifiers
1. 860
/organism="Mus musculus"
/mol_type="mRNA"
/strain="PVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4981433"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NCI CGAP Co24"
/note="Organ: NCI CGAP Co24"
Site 2: Sail; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 90.0%; Score 18; DB 2; Length 860;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGTC 18
|||||
Db 179 TTGACCCCGCCCTGTGTC 196

RESULT 3
CZ741905 332 bp DNA linear GSS 26-JUL-2005
LOCUS OC_Ba0088D18.f OC_Ba Oryza coarctata genomic clone OC_Ba0088D18
DEFINITION 5'__genomic survey sequence.
ACCESSION CZ741905
VERSION CZ741905.1 GI:71173260
KEYWORDS GSS.

SOURCE Oryza coarctata (Porteresia coarctata)
ORGANISM Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzaceae; Oryza.
1 (bases 1 to 332)
Kim, H., Collura, K., Wisotsakul, M., Byrne, M., Scum, D., Smart, D.,
Rao, K., Luo, M., Jettly, R., Kudrna, D., Muller, C., Soderlund, C. and
Wing, R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0088 row: D column: 18
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
1. 332
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0088D18"
/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_1ib="OC_Ba"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 332;
Best Local Similarity 94.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGACCCCGCCCTGTGTC 20
|||||
Db 297 TGACCCCGCCCTGTGTC 279

RESULT 4
DR752859 479 bp mRNA linear EST 21-JUL-2005
LOCUS CYMG2P07 Coprinus cinereus YMG medium exponentially growing
DEFINITION mycelia cDNAs Coprinopsis cinerea cDNA, mRNA sequence.
ACCESSION DR752859
VERSION DR752859.1 GI:71045301
KEYWORDS EST.
SOURCE Coprinopsis cinerea (Coprinus cinereus)
ORGANISM Coprinopsis cinerea
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Psathyrellaceae; Coprinopsis.
1 (bases 1 to 479)
Wilke, S.K., Carlson, M.D., Barr, C., Murphy, B., Peters, J.M.,
Guerrero, A.R., Gathman, A.C., Lilly, W.W. and Pukkila, P.J.
Expressed sequence tags from Coprinus cinereus (Coprinopsis
cinerea) cDNAs, summer 2005
Unpublished (2005)
Contact: Gathman AC
Biology Department
Southeast Missouri State University
1 University Plaza, Cape Girardeau, MO 63701, USA
Tel: 5736512361
Fax: 573 651 2382
Email: agathman@semo.edu
Location/Qualifiers
1. 479

FEATURES
source

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 479;
 Best Local Similarity 94.7%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGACCCCGCCCTGTGCTG 20
 Db 17 TTGACCCCGCCCGAGGTCTG 35

/organism="Coprinopsis cinerea"
 /mol_type="mRNA"
 /strain="Okayama7#130"
 /db_xref="taxon:5346"
 /dev_stage="vegetative monokaryotic mycelium"
 /lab_host="E. coli XL10-Gold"
 /clone_lib="Coprinus cinereus YMG medium exponentially growing mycelia cDNA"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; Mycelia grown for three days at 37 degrees on YMG medium."

RESULT 5
 BP153423
 LOCUS BP153423 full-length enriched swine CDNA library, adult ovary Sus
 DEFINITION BP153423 scrofa cDNA clone OVRM10124G10 5', mRNA sequence.
 ACCESSION BP153423
 VERSION BP153423.1 GI:40402896
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus

REFERENCE 1 (bases 1 to 606)
 AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.
 TITLE PBDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
 JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
 PUBMED 14681463
 COMMENT Contact: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STRAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.

FEATURES

Location/Qualifiers
 1..606
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="OVRM10124G10"
 /tissue_type="ovary"
 /dev_stage="adult"
 /clone_lib="full-length enriched swine CDNA library, adult ovary"

ORIGIN

Query Match 87.0%; Score 17.4; DB 3; Length 606;
 Best Local Similarity 94.7%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCTG 19
 Db 61 TTGACCCCGCCCTGTGCTG 79

RESULT 6
 BH342849
 LOCUS BH342849 661 bp DNA linear GSS 03-DEC-2001
 DEFINITION CH230-41L14.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-41L14, genomic survey sequence.
 ACCESSION BH342849
 VERSION BH342849.1 GI:17273583
 KEYWORDS GSS.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 661)
 AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsagaye,G., Geer,K., Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
 TITLE Rat BAC End Sequences from Library CHORI-230 EcORI segment Unpublished (1999)
 JOURNAL Other_GSS: CH230-41L14.TV
 COMMENT Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cno.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering_information.html). BAC end plates: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 41 row: L column: 14
 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..661
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SavHsd/MCM"
 /db_xref="taxon:10116"
 /clone="CH230-41L14"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 1"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; CHORI-230 Rat (BN/SavHsd/MCM) BAC library produced by Pieter de Jong"

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 661;
 Best Local Similarity 94.7%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCTG 19
 Db 225 TTGACCCCGCCCTGTGCTG 243

RESULT 7
 BH342931
 LOCUS BH342931 665 bp DNA linear GSS 03-DEC-2001
 DEFINITION CH230-41L4.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-41L4, genomic survey sequence.
 ACCESSION BH342931
 VERSION BH342931.1 GI:17273665
 KEYWORDS GSS.

SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 665)
Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcORI segment
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Other-GSSs: CH230-41L4.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering-information.html>). BAC end
page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 41 row: 1 column: 4
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..665
location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-41L4"
/sex="Female"
/cell_type="Brain"
/clone_1lb="CHORI-230 Segment 1"
/note="Vector: pTARAC2.1; Site 1: EcORI; Site 2: EcORI;
CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 87.0%; Score 17.4; DB 9; Length 665;
Best Local Similarity 94.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 TTGACCCCGCCCTGTCG 19
|||||
242 TTGACCCCGCCCTGTCG 260

Db
242 TTGACCCCGCCCTGTCG 260

RESULT 8
CNS03391 959 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION
Tetradon nigriviridis genome survey sequence PUC-Orl end of clone
208H03 of library G from Tetradon nigriviridis, genomic survey
sequence.
ACCESSION
AL225838
VERSION
AL225838.1 GI:7884744
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetradon nigriviridis
ORGANISM
Tetradon nigriviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE
AUTHORS
1
Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fitzames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigriviridis DNA sequence

JOURNAL
PUBMED
REFERENCE
AUTHORS
2
Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
Fitzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigriviridis
Genome Res. 10 (7), 939-949 (2000)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
3 (bases 1 to 959)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigriviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetradon>.

FEATURES
source
1..959
location/Qualifiers
/organism="Tetradon nigriviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="208H03"
/clone_1lb="G"
/note="Genoscope sequence ID : COAG208CD02SP1
end : PUC-Orl"

ORIGIN
Query Match 87.0%; Score 17.4; DB 11; Length 959;
Best Local Similarity 94.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 TTGACCCCGCCCTGTCG 19
|||||
255 TTGACCCCGCCCTGTCG 273

Db
255 TTGACCCCGCCCTGTCG 273

RESULT 9
CNS041R0 336 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION
Tetradon nigriviridis genome survey sequence T7 end of clone
075A13 of library G from Tetradon nigriviridis, genomic survey
sequence.
ACCESSION
AL270549
VERSION
AL270549.1 GI:7992474
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetradon nigriviridis
ORGANISM
Tetradon nigriviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE
AUTHORS
1
Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fitzames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigriviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
2
Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
Fitzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigriviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL
PUBMED
REFERENCE
AUTHORS
3 (bases 1 to 336)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetradon>.

FEATURES
 source
 1..336
 /organism="Tetradon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="075A13"
 /clone_1ib="G"
 /note="Genoscope sequence ID : C0BG075AA07LP1
 end : 17"

ORIGIN
 Query Match 85.0%; Score 17; DB 11; Length 336;
 Best Local Similarity 89.5%; Pred. No. 3.4e+03;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy
 1 TTGACCCCGCCCTGTCTG 19
 |||||
 205 TTACCCCGCCCTGTCTG 223

RESULT 10
LOCUS B1751547/c 438 bp mRNA linear EST 25-SEP-2001

DEFINITION Ta01_19e09 R
 Ta01_AAFc ECORC Fusarium graminearum inoculated wheat heads
 Triticum aestivum cDNA clone Ta01_19e09, mRNA sequence.

ACCESSION B1751547
VERSION B1751547.1 GI:15773349
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 438)
 Ouellet,T., Dan,H., Koul,A., Chapados,J., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
 Expressed Sequence Tags from Wheat Heads 24 Hours after Spray Inoculation with Fusarium graminearum
 Unpublished (2001)
 Contact: Ouellet, Therese
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 Neaby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA
 Tel: (613) 759-1658
 Fax: (613) 759-1701
 Email: ouellet@agr.gc.ca.

JOURNAL Unpublished (2001)
COMMENT Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 Neaby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA
 Tel: (613) 759-1658
 Fax: (613) 759-1701
 Email: ouellet@agr.gc.ca.

FEATURES
 source
 1..438
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Frontana"
 /db_xref="taxon:4565"
 /clone="Ta01_19e09"
 /clone_1ib="G"
 /dev_stage="anthesis"
 /tissue_type="heads"
 /clone_1ib="Ta01_AAFc_ECORC_Fusarium_graminearum_inoculated_wheat_heads"
 /note="Vector: pGEM-T easy; Site 1: EcoRI, Site 2: EcoRI; Controlled chamber-grown wheat heads were spray inoculated at mid-anthesis with a Fusarium graminearum macroconidial suspension (50,000 spores/ml) and kept under intermittent misting for 24 hours, then collected and immediately

ORIGIN
 frozen in liquid nitrogen."

Query Match 85.0%; Score 17; DB 3; Length 438;
 Best Local Similarity 89.5%; Pred. No. 3.4e+03;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy
 1 TTGACCCCGCCCTGTCTG 19
 |||||
 425 TTGACCCCGCCCTGTCTG 407

RESULT 11
LOCUS B153575 499 bp mRNA linear EST 30-NOV-2001

DEFINITION TCBAp2D9954 Pediatric pre-B cell acute lymphoblastic leukemia
 Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAp9954, mRNA sequence.

ACCESSION B153575
VERSION B153575.1 GI:17178843
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 499)
 Wei,Y., Teang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R., Jr., Gunaratne,P.H., Muzny,D., Bouck,Y., Gibbs,R.A. and Margolin,J.F.
 Pediatric Leukemia cDNA Sequencing Project (2001)
 Unpublished (2001)
 Contact: Dr. Judith F. Margolin
 Texas Children's Cancer Center and Human Genome Sequencing Center
 at Baylor College of Medicine
 1102 Bates, MC3-3320 Houston, TX 77030, USA
 Tel: 832-824-4536
 Fax: 832-825-4038
 Email: clones@tccc.org
 Seq primer: M13 primer.

JOURNAL Unpublished (2001)
COMMENT Texas Children's Cancer Center and Human Genome Sequencing Center
 at Baylor College of Medicine
 1102 Bates, MC3-3320 Houston, TX 77030, USA
 Tel: 832-824-4536
 Fax: 832-825-4038
 Email: clones@tccc.org
 Seq primer: M13 primer.

FEATURES
 source
 1..499
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TCBAp9954"
 /sex="male"
 /tissue_type="leukophereis"
 /cell_type="pre-B cell"
 /dev_stage="pediatric 2 years"
 /lab_host="DH10B"
 /clone_1ib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"
 /note="Vector: lambda pSB; Site 1: BamHI, Site 2: EcoRI; First strand cDNA was primed with an anchored xhoi-oligo(dT) primer [5'GGAGAGCTCGAGCGCGGAGAGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGATCGCGCGGAGATTAATTAAT(C) 3']. Double-stranded cDNA was then digested with BamI and XhoI and directionally cloned into the BamI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P. Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

ORIGIN
 Query Match 85.0%; Score 17; DB 3; Length 499;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGCT 17
 |||||
 Db 279 TTGACCCCGCCCTGCT 295
 |||||

RESULT 12
 A1671109 214 bp mRNA linear EST 18-MAY-1999
 LOCUS wbj3c05.x1 NCI CGAP GC6 Homo sapiens CDNA IMAGE:2305544 3'
 DEFINITION similar to TR:Q43582 Q43582 GLYCINE RICH PROTEIN. ;, mRNA sequence.
 A1671109
 ACCESSION A1671109.1 GI:4850840
 VERSION EST.
 KEYWORDS Homo sapiens
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 214)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2305544"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_11b="NCI CGAP GC6"
 /note="Vector: pT735-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP GC4 was prepared, and
 as circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 " "

ORIGIN
 Query Match 84.0%; Score 16.8; DB 1; Length 214;
 Best Local Similarity 90.0%; Pred. No. 4.3e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGCT 20
 |||||
 Db 60 TTGACCCCGCCCTGACGT 79
 |||||

RESULT 13
 CW754796 310 bp DNA linear GSS 09-NOV-2004
 LOCUS CG_BBa0057A15.r OG_BBa Oryza glaberrima genomic clone OG_BBa0057A15
 DEFINITION 3', genomic survey sequence.
 CW754796
 ACCESSION

VERSION CW754796.1 GI:55593454
 KEYWORDS GSS.
 SOURCE Oryza glaberrima (African rice)
 ORGANISM Oryza glaberrima
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 310)
 Kim,H., Yu,Y., Wasecaki,M., Byrne,M., Stum,D., Smart,D., Rao,K.,
 Luo,M., Jettly,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.
 and Wing,R.
 OMAP
 Unpublished (2004)
 CONTACT: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1255
 Email: rwing@genome.arizona.edu
 PCR PRIMERS
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0057 row: A column: 15
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.
 Location/Qualifiers
 1..310
 /organism="Oryza glaberrima"
 /mol_type="genomic DNA"
 /db_xref="taxon:4538"
 /clone="OG_BBa0057A15"
 /tissue_type="Young leaves"
 /lab_host="DH10B T1 phage resistant"
 /clone_11b="OG_BBa"
 /note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"
 " "

ORIGIN
 Query Match 84.0%; Score 16.8; DB 10; Length 310;
 Best Local Similarity 90.0%; Pred. No. 4.2e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGCT 20
 |||||
 Db 136 TGGACCCGACCCCTGCTGCT 155
 |||||

RESULT 14
 A1882346 426 bp mRNA linear EST 22-JUL-1999
 LOCUS ub99b09.x1 Soares_mammary_gland NBMWG Mus musculus CDNA clone
 DEFINITION IMAGE:1396601 5', mRNA sequence.
 A1882346
 ACCESSION A1882346.1 GI:5567435
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 426)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:908317
 Seq primer: -28m3 rev2 ET from Amersham
 High quality sequence stop: 411.
 Location/Qualifiers

FEATURES

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 14:51:10 ; Search time 219.5 Seconds
(without alignments)
607.261 Million cell updates/sec

Title: US-10-696-708a-61

Perfect score: 20

Sequence: 1 ttgaccccccgcctgcgtcgt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAA07659 Reverse p
2	16.8	84.0	1017	8	ACA19614 Prokaryot
3	16.8	84.0	1026	11	ABD04465 Pseudomon
4	16.8	84.0	1053	11	ABD04362 Pseudomon
5	16.8	84.0	1617	11	ABD04301 Pseudomon
6	16.4	82.0	890	13	ADK63316 Plant ful
7	16.4	82.0	1124	13	ADK49634 Plant ful
8	16.4	82.0	1483	13	ADK46563 Plant ful
9	15.8	79.0	501	11	ABD04697 Pseudomon
10	15.8	79.0	735	6	ABN90562 Staphyloc
11	15.8	79.0	819	6	ABN90564 Staphyloc
12	15.8	79.0	1008	4	AAS54373 Pseudomon
13	15.8	79.0	1020	11	ABD03622 Pseudomon
14	15.8	79.0	1038	11	ABD03697 Pseudomon
15	15.8	79.0	1221	11	ABD04007 Pseudomon
16	15.8	79.0	1842	8	ADA71243 Rice gene
17	15.8	79.0	1965	11	ABD04630 Pseudomon
18	15.8	79.0	1980	3	AAZ51001 X. oryzae
19	15.8	79.0	2000	8	ADA72201 Rice gene

C 20	15.8	79.0	2093	4	AA501678 Human T-t
C 21	15.8	79.0	2325	11	ABD04809 Pseudomon
C 22	15.8	79.0	2763	8	ACC42478 Human C1Q
C 23	15.8	79.0	2803	12	ADO22316 Human sof
C 24	15.8	79.0	3431	8	ABZ34816 Coding se
C 25	15.8	79.0	3431	13	ACN37667 Tumour-as
C 26	15.8	79.0	3667	14	ADV70146 Tumor-ab
C 27	15.8	79.0	3720	3	AAZ51000 X. oryzae
C 28	15.8	79.0	3954	3	AAZ51000 X. oryzae
C 29	15.8	79.0	5846	4	AAZ51000 X. oryzae
C 30	15.8	79.0	5846	8	ADA41544 Human sec
C 31	15.8	79.0	5846	8	ACC50892 Human sec
C 32	15.8	79.0	5846	8	ABX59942 CDNA enco
C 33	15.8	79.0	5846	10	ADCT74643 Human sec
C 34	15.8	79.0	5846	10	ADCT74643 Human sec
C 35	15.8	79.0	5846	10	ADA57675 BAC fragm
C 36	15.8	79.0	5846	12	ADJ30692 Human mus
C 37	15.8	79.0	5848	4	AAZ51000 X. oryzae
C 38	15.8	79.0	5848	8	ADA41545 Human sec
C 39	15.8	79.0	5848	8	ACC50893 Human sec
C 40	15.8	79.0	5848	8	ABX59943 CDNA enco
C 41	15.8	79.0	5848	10	ADCT74644 Human sec
C 42	15.8	79.0	5848	10	ADD38113 CDNA c1on
C 43	15.8	79.0	5848	10	ADA57676 BAC fragm
C 44	15.8	79.0	5848	12	ADJ30693 Human mus
C 45	15.8	79.0	12423	10	ADB53947 CACNA1G g

ALIGNMENTS

RESULT 1
ID AAA07659 standard; DNA; 20 BP.
AC AAA07659;

DT 19-JUN-2000 (first entry)

DE Reverse primer for amplifying HERG gene exon 2.

KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; human;

KW PCR primer; ss.

OS Homo sapiens.

PN WO200006772-A1.

PD 10-FEB-2000.

PF 20-JUL-1999; 99WO-US016337.

PR 27-JUL-1998; 98US-00122847.

PR 06-JAN-1999; 99US-00226012.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

DR WPI; 2000-195319/17.

PT New isolated mutant HERG nucleic acids, useful for developing products

PT for the diagnosis, prevention and treatment of long QT syndrome.

PS Claim 7; Page 72; 163p; English.

The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of subjects with LQT syndrome. CC can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and CC HERG peptides can be used for peptide therapy. Sequences AAA07654-693

CC represent primers for amplifying HERG exons
 XX Sequence 20 BP; 1 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTGACCCCGCCCTGTGCT 20
 1 TTGACCCCGCCCTGTGCT 20
 Db 1 TTGACCCCGCCCTGTGCT 20

RESULT 2
 ACA19614/c
 ID ACA19614 standard; DNA; 1017 BP.
 XX
 AC ACA19614;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #1271.
 XX
 KM Antisense; ds; prokaryotic essential gene; cell proliferation;
 KM drug design; gene.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN WO20027183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELITR) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI: 2003-029926/02.
 DR P-PSDB; ABU15744.
 XX
 PT New antisense nucleic acid, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation or
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 7484; 1766bp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences
 XX
 SQ Sequence 1017 BP; 205 A; 325 C; 333 G; 154 T; 0 U; 0 Other;
 QY Query Match 84.0%; Score 16.8; DB 8; Length 1017;
 Best Local Similarity 90.0%; Pred. No. 4.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 1 TTGACCCCGCCCTGTGCT 20
 608 TTGACCCCGCCCTGTGCT 589

RESULT 3
 ABD04465/c
 ID ABD04465 standard; DNA; 1026 BP.
 XX
 AC ABD04465;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polynucleotide #3069.
 XX
 KM Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KM antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI WPI: 2003-615309/58.
 XX
 DR P-PSDB; ABO70894.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 3069; 455bp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
 CC infection, and in detection of *P. aeruginosa* sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-

CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1026 BP, 208 A, 327 C, 335 G, 156 T, 0 U, 0 Other;

Query Match 84.0%; Score 16.8; DB 11; Length 1026;
Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGCT 20
DB 617 TTGACCCCGCCCTGTGCT 598

RESULT 4
ABD04362/C
ID ABD04362 standard; DNA, 1053 BP.

AC ABD04362;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #2966.

KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
antibacterial.

OS Pseudomonas aeruginosa.

PN US651795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR P-PSDB; ABO70791.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 2966; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABD01397-
XX ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html

SQ Sequence 1053 BP, 218 A, 338 C, 340 G, 157 T, 0 U, 0 Other;

Query Match 84.0%; Score 16.8; DB 11; Length 1053;

Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGCT 20
DB 600 TTGACCCCGCCCTGTGCT 581

RESULT 5
ABD04301
ID ABD04301 standard; DNA, 1617 BP.

AC ABD04301;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #2905.

KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
antibacterial.

OS Pseudomonas aeruginosa.

PN US651795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR P-PSDB; ABO70730.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 2905; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABD01397-
XX ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html

SQ Sequence 1617 BP, 239 A, 555 C, 516 G, 307 T, 0 U, 0 Other;

Query Match 84.0%; Score 16.8; DB 11; Length 1617;
Best Local Similarity 90.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGCT 20
DB 653 TTGACCCCGCCCTGTGCT 672

RESULT 6
 ADX63316
 ID ADX63316 standard; cDNA; 890 BP.
 XX
 AC ADX63316;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 34159.
 XX
 KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 PN US200403488-A1.
 XX
 PD 19-FEB-2004.
 XX
 PP 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/J) LIU J.
 PA (ZHOU/J) ZHOU Y.
 PA (KOVA/J) KOVALIC D K.
 PA (SCRE/J) SCREEN S E.
 PA (TABAK/J) TABASKA J E.
 PA (CAO/Y) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI: 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 34159; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX
 SQ Sequence 890 BP; 172 A; 243 C; 256 G; 219 T; 0 U; 0 Other;
 Query Match 82.0%; Score 16.4; DB 11; Length 890;
 Best Local Similarity 94.4%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGACCCCGCCCTGTCG 19
 DB 36 TGACCCCGCTCTGTCG 53
 RESULT 7
 ADX49634
 ID ADX49634 standard; cDNA; 1124 BP.
 XX
 AC ADX49634;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 24374.
 XX
 KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 PN US200403488-A1.
 XX
 PD 19-FEB-2004.
 XX
 PP 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/J) LIU J.
 PA (ZHOU/J) ZHOU Y.
 PA (KOVA/J) KOVALIC D K.
 PA (SCRE/J) SCREEN S E.
 PA (TABAK/J) TABASKA J E.
 PA (CAO/Y) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI: 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 24374; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX
 SQ Sequence 1124 BP; 238 A; 294 C; 286 G; 306 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 13; Length 1124;
Best Local Similarity 94.4%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGCTCG 19
|||||
Db 55 TGACCCCGCTCTGCTCG 72

RESULT 8
ADx46563
ID ADx46563 standard; cDNA; 1483 BP.
XX
AC ADx46563;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 21303.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAJ/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 21303; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1483 BP; 305 A; 418 C; 399 G; 361 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 13; Length 1483;
Best Local Similarity 94.4%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGCTCG 19
|||||
Db 574 TGACCCCGCTCTGCTCG 591

RESULT 9
ABD04697
ID ABD04697 standard; DNA; 501 BP.
XX
AC ABD04697;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #3301.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
XX
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
XX
DR P-PSDB; ABO71126.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 3301; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC segdata.uspto.gov/sequence.html
XX
SQ Sequence 501 BP; 77 A; 177 C; 160 G; 87 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 501;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGACCCCGCCCTGGTCT 20
Db 305 TGCCCCCGCCGTGTCT 323

RESULT 10
ABN90562
ID ABN90562 standard; DNA; 735 BP.

XX ABN90562;

XX 24-JUL-2002 (first entry)

XX Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:25.

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX antibacterial; gene therapy; gene; ds.

XX Staphylococcus epidermidis.

XX US6380370-B1.

XX 30-APR-2002.

XX 13-AUG-1998; 98US-00134001.

XX 14-AUG-1997; 97US-0055779P.

XX 08-NOV-1997; 97US-0064964P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Doucet-Stamm LA, Bush D;

XX WPI; 2002-381255/41.

XX P-PSDB; ABP38017.

XX Novel isolated nucleic acid encoding a Staphylococcus epidermis

XX polypeptide, useful for diagnosing and treating bacterial infections.

XX Disclosure; SEQ ID NO 25; 267bp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading

XX frame (ORF) nucleic acid sequences which encode the amino acid sequences

XX given in ABP3124 to ABP37960. The S. epidermidis sequences have

XX antibacterial activity and can be used in gene therapy. The sequences can

XX also be used in the diagnosis and treatment of bacterial infections,

XX particularly S. epidermidis infections. The sequences can be used to

XX screen for compounds able to interfere with the S. epidermidis life cycle

XX or inhibit S. epidermidis infection. N.B. The sequence data for this

XX patent did not form part of the printed specification, but was obtained

XX in electronic format directly from the USPTO web site

XX Sequence 735 BP; 121 A; 250 C; 237 G; 127 T; 0 U; 0 Other;

XX Query Match 79.0%; Score 15.8; DB 6; Length 735;

XX Best Local Similarity 89.5%; Pred. NO. 1.3e+03;

XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1 TTGACCCCGCCCTGGTCT 19

XX 221 TTGACCCCGCCCTGGCG 239

Db

RESULT 11

ABN90564/C

XX ABN90564 standard; DNA; 819 BP.

XX ABN90564;

XX 24-JUL-2002 (first entry)

XX

DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:27.

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX antibacterial; gene therapy; gene; ds.

XX Staphylococcus epidermidis.

XX US6380370-B1.

XX 30-APR-2002.

XX 13-AUG-1998; 98US-00134001.

XX 14-AUG-1997; 97US-0055779P.

XX 08-NOV-1997; 97US-0064964P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Doucet-Stamm LA, Bush D;

XX WPI; 2002-381255/41.

XX P-PSDB; ABP38019.

XX Novel isolated nucleic acid encoding a Staphylococcus epidermis

XX polypeptide, useful for diagnosing and treating bacterial infections.

XX Disclosure; SEQ ID NO 27; 267bp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading

XX frame (ORF) nucleic acid sequences which encode the amino acid sequences

XX given in ABP3124 to ABP37960. The S. epidermidis sequences have

XX antibacterial activity and can be used in gene therapy. The sequences can

XX also be used in the diagnosis and treatment of bacterial infections,

XX particularly S. epidermidis infections. The sequences can be used to

XX screen for compounds able to interfere with the S. epidermidis life cycle

XX or inhibit S. epidermidis infection. N.B. The sequence data for this

XX patent did not form part of the printed specification, but was obtained

XX in electronic format directly from the USPTO web site

XX Sequence 819 BP; 144 A; 261 C; 274 G; 140 T; 0 U; 0 Other;

XX Query Match 79.0%; Score 15.8; DB 6; Length 819;

XX Best Local Similarity 89.5%; Pred. NO. 1.3e+03;

XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1 TTGACCCCGCCCTGGTCT 19

XX 524 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

XX 221 TTGACCCCGCCCTGGCG 506

PR 26-MAY-2000; 2000US-0207722P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELITR) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr CJ,
PI Yamamoto RT, Xu HH;
XX
DR WPI, 2001-611495/70.
DR P-PSDB; AA036514.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 27; SEQ ID NO 8010; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC *coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1008 BP; 169 A; 370 C; 305 G; 164 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 4; Length 1008;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCGCGCCCTGTGTCG 19
Db 922 TTGACCGCGCCCTGTGTCG 940

RESULT 13
ABD03622
ID ABD03622 standard; DNA; 1020 BP.
XX
AC ABD03622;
XX
DT 29-JUL-2004 (first entry)
XX
DE *Pseudomonas aeruginosa* polynucleotide #2226.
XX
KW Bacterial infection; gene; ds; *Pseudomonas aeruginosa* infection;
KW antibacterial.
XX
OS *Pseudomonas aeruginosa*.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PT

PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI, 2003-615309/58.
DR P-PSDB; AB070051.
XX
XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 2226; 455pp; English.
XX
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biotech technology. Sequences ABD01397-
CC ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1020 BP; 173 A; 387 C; 297 G; 163 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 1020;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCGCGCCCTGTGTCG 19
Db 995 TTGACCGCGCCCTGTGTCG 1013

RESULT 14
ABD03697
ID ABD03697 standard; DNA; 1038 BP.
XX
AC ABD03697;
XX
DT 29-JUL-2004 (first entry)
XX
DE *Pseudomonas aeruginosa* polynucleotide #2301.
XX
KW Bacterial infection; gene; ds; *Pseudomonas aeruginosa* infection;
KW antibacterial.
XX
OS *Pseudomonas aeruginosa*.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI, 2003-615309/58.
DR P-PSDB; AB070126.
XX
XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,

PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 2301; 455bp; English.
XX
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences ABD01397-
CC ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1038 BP; 179 A; 384 C; 308 G; 167 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 1038;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGTCG 19
DB 952 TTGACCCCTGCGCCCTGTGTCG 970

RESULT 15
ABD04007/C
ID ABD04007 standard; DNA; 1221 BP.
XX
AC ABD04007;
XX
DT 29-JUL-2004 (first entry)
XX
DE *Pseudomonas aeruginosa* polynucleotide #2611.
XX
KM Bacterial infection; gene; ds; *Pseudomonas aeruginosa* infection;
XX antibacterial.
XX
OS *Pseudomonas aeruginosa*.
XX
FN US6551795-B1.
XX
PD 22-APR-2003.
XX
PE 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
FI Rubenfeld MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
XX P-PSDB; ABO70436.
XX
PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 2611; 455bp; English.
XX
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,

CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences ABD01397-
CC ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1221 BP; 210 A; 353 C; 437 G; 221 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 1221;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGTCG 19
DB 186 TTGACCCCTGCGCCCTGTGTCG 168

Search completed: April 10, 2006, 15:24:14
Job time : 221.5 secs

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 14:56:10 ; Search time 1128.5 Seconds
(without alignments)
1007.416 Million cell updates/sec

Title: US-10-696-708A-61

Perfect score: 20
Sequence: 1 ttgaccccgccctgctcgt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_bcs:*
11: gb_by:*
12: gb_un:*
13: gb_vl:*
14: gb_hrg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	20	100.0	20	AR139544	AR139544 Sequence
2	20	100.0	20	BD223633	BD223633 Mutations
3	20	100.0	20	CS124259	CS124259 Sequence
4	20	100.0	16879	AC011234	AC011234 Homo sapi
5	20	100.0	181369	AC146440	AC146440 Pan trogl
6	20	100.0	216408	AC092466	AC092466 Homo sapi
7	18.4	92.0	331	HS010538	AJ010538 Homo sapi
8	17.4	87.0	110000	BA000030	Continuation (63 o
9	17.4	87.0	110000	AC150790	Continuation (2 of
10	17.4	87.0	155060	AC140158	AC140158 Felis cat
11	17.4	87.0	156383	AC135221	AC135221 Felis cat
12	17.4	87.0	212682	AC157414	AC157414 Bos tauru
13	17.4	87.0	218381	AC150564	AC150564 Bos tauru
14	17.4	87.0	243300	AC098101	AC098101 Rattus no
15	17	85.0	236135	AC150514	AC150514 Bos tauru
16	17	85.0	26583	AC111344	AC111344 Rattus no
17	16.8	84.0	1196	AJ844245	AJ844245 Tarphius
18	16.8	84.0	1196	AJ844247	AJ844247 Tarphius

19	16.8	84.0	1196	2	AJ844248	AJ844248 Tarphius
20	16.8	84.0	1196	2	AJ844250	AJ844250 Tarphius
21	16.8	84.0	1196	2	AJ844251	AJ844251 Tarphius
22	16.8	84.0	1196	2	AJ844252	AJ844252 Tarphius
23	16.8	84.0	3143	1	PSEFLIE	143507 Pseudomona
24	16.8	84.0	15833	1	AB004540	AB004540 Pseudomon
25	16.8	84.0	101215	8	AC006966	AC006966 Homo sapi
26	16.8	84.0	106100	14	AC119405	AC119405 Magnapor
27	16.8	84.0	108523	8	AC000159	AC000159 Homo sapi
28	16.8	84.0	110000	1	CP000089	CP000089 Dechlorom
29	16.8	84.0	110000	14	AC073702	Continuation (4 of
30	16.8	84.0	110000	15	AP008207	Continuation (340
31	16.8	84.0	110000	15	AP008209	Continuation (52 o
32	16.8	84.0	128809	14	AC105931	AC105931 Magnapor
33	16.8	84.0	135237	14	AP000814	AP000814 Homo sapi
34	16.8	84.0	149775	5	BX276127	BX276127 Zebrafish
35	16.8	84.0	155037	15	AC116426	AC116426 Genomic B
36	16.8	84.0	161970	15	AP003221	AP003221 Oryza sat
37	16.8	84.0	164309	14	BX927084	BX927084 Dantio rer
38	16.8	84.0	166497	15	AP003293	AP003293 Oryza sat
39	16.8	84.0	171793	8	AP001187	AP001187 Homo sapi
40	16.8	84.0	171980	14	AP000928	AP000928 Homo sapi
41	16.8	84.0	178100	14	AP001558	AP001558 Homo sapi
42	16.8	84.0	180276	14	AC162724	AC162724 Papio anu
43	16.8	84.0	181163	15	AC115687	AC115687 Genomic B
44	16.8	84.0	187483	14	AC090316	AC090316 Homo sapi
45	16.8	84.0	189857	14	AC128637	AC128637 Rattus no

ALIGNMENTS

RESULT 1	AR139544	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR139544	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 16-JUN-2001
DEFINITION	AR139544	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 16-JUN-2001
ACCESSION	AR139544	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 16-JUN-2001
VERSION	AR139544.1	GI:14482040	20 bp	DNA	linear	PAT 16-JUN-2001
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
	/mol_type="unassigned DNA"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 2	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
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Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 3	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 4	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 5	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 6	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 7	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 8	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 9	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					
Db	1 TTGACCCCGCCCTGCTGCT 20					
RESULT 10	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD223633	Sequence 61 from patent US 6207383.	20 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD223633.1	GI:33033403	20 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	JP 2002521065-A/59.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Keating,M.T. and Splawski,I.					
TITLE	Mutations in and genomic structure of HERG--a long QT syndrome gene					
JOURNAL	Patent: US 6207383-A 61 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
ORIGIN	/organism="Unknown"					
Query Match	100.0%;	Score 20;	DB 6;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 TTGACCCCGCCCTGCTGCT 20					

RESULT 4	AC011234/c	16879 bp	DNA	linear	PRI 31-JAN-2000
LOCUS	AC011234	16879 bp	DNA	linear	PRI 31-JAN-2000
DEFINITION	Homo sapiens BAC clone RP11-166D23	from 7, complete sequence.			
ACCESSION	AC011234				
VERSION	AC011234.2	GI:7684547			
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1 (bases 1 to 16879)				
AUTHORS	Hallier,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H.,				
	Wagner-McPherson,C., Layman,D., Maas,J., Jaeger,S., Walker,R.,				
	Wylie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.E.,				
	Reuell,G.A., Delehanty,K.D., Miner,T.L., Nash,W.F., Cordes,M.,				
	Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S.,				
	Isak,A., Vamburum,A., Nguyen,C., Du,F., Lamar,B., Courtney,L.,				
	Kalicki,J., Ozeran,P., Strong,C.M., Scott,K., Holmes,A.,				
	Hackins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C.,				
	Daphin-Vohberg,S., Kozlowski-Reilly,A., Leonard,J.D., Rohlfing,T.,				
	Rock,S.M., Tin-Wollam,A.M., Abbott,A., Mix,P., Maupin,R.,				
	Stromwalt,C., Latreille,P., Miller,N., Johnson,D., Marry,J.,				
	Wessner,J.P., Wend,M.C., Yang,S.P., Schultz,B.R., Wallis,J.W.,				
	Speeth,J., Bieri,T.A., Nelson,J.O., Berkowicz,N., Wohlmann,P.E.,				
	Cook,L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,J.A.,				
	Mardis,E.R., Clifton,S.W., Chisoe,S.L., Merra,M.A., Raymond,C.,				
	Haugen,E., Gillett,W., Zhou,Y., James,R., Phelps,K., Iadonco,S.,				
	Bubb,K., Simms,E., Levy,R., Clendenning,J., Kaul,R., Kent,W.J.,				
	Purey,T.S., Baertsch,R.A., Brent,M.R., Keldler,E., Plicek,P.,				
	Boek,P., Suyama,M., Bailey,J.A., Portnoy,M.E., Torrents,D.,				
	Chinwalla,A.T., Ghis,W.R., Eddy,S.R., McPherson,J.D., Olson,M.V.,				
	Elchler,E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.				
	The DNA sequence of human chromosome 7				
TITLE	Nature 424 (6945), 157-164 (2003)				
JOURNAL	12853948				
REFERENCE	2 (bases 1 to 16879)				
AUTHORS	Harkins,R., Lamar,B. and Stoneking,T.				
TITLE	The sequence of Homo sapiens BAC clone RP11-166D23				
JOURNAL	Unpublished (2001)				
REFERENCE	3 (bases 1 to 16879)				
AUTHORS	Waterston,R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-OCT-1999) Genome Sequencing Center, Washington				
	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
	MO 63108, USA				
REFERENCE	4 (bases 1 to 16879)				
AUTHORS	Waterston,R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-MAY-2000) Genome Sequencing Center, Washington				
	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
	MO 63108, USA				
REFERENCE	6 (bases 1 to 16879)				
AUTHORS	Waterston,R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-JUN-2000) Genome Sequencing Center, Washington				
	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
	MO 63108, USA				
REFERENCE	7 (bases 1 to 16879)				
AUTHORS	Waterston,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-SEP-2000) Department of Genetics, Washington				
	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA				
REFERENCE	8 (bases 1 to 16879)				

AUTHORS Wilson, R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On May 3, 2000 this sequence version replaced gi:6007897.

----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu>
 Contact: sapiens@wuston.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0166D23

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:
 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Ososogawa, K., Moon, P. Y., Zhao, B., Frenken, E., Tatem, M., Cataneese, J. J. and de Jong, P. J. (1996) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-148K1 the clone sequenced to the right is RP4-548K24, 200 base pair overlap. Actual end of this clone is at base position 77856 of RP4-548K24.

FEATURES

SOURCE
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 484..974
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 1018..1075
 /rpt_family="L2"
 1208..1586
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 1590..1638
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 1824..1874
 /rpt_family="CT-rich"
 3792..5639
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 repeat_region 4861..4956
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 5060..5131
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 repeat_region 5174..5347
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 Continues as H_DJ0548K24.1.1"
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 repeat_region 9417..9531
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 Best Local Similarity 100.0%; Pred. No. 1,4e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTGACCCCGCCCGTGTGT 20
 Db 8622 TTGACCCCGCCCGTGTGT 8603
 RESULT 5
 AC146440 AC146440 181369 bp DNA linear PRI 18-AUG-2004
 LOCUS
 DEFINITION Pan troglodytes BAC clone RP43-11P1 from 7, complete sequence.
 ACCESSION AC146440

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VERSION      AC146440.5  GI:50204414
KEYWORDS     HTG.
SOURCE       Pan troglodytes (chimpanzee)
ORGANISM     Pan troglodytes
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Pan.
REFERENCE    1 (bases 1 to 181369)
AUTHORS     Shah,N. and Bielecki,L.
TITLE       The sequence of Pan troglodytes BAC clone RP43-11P11
JOURNAL     Unpublished (2001)
REFERENCE    2 (bases 1 to 181369)
AUTHORS     Wilson,R.K.
TITLE       Direct Submission
JOURNAL     Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
              Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE    3 (bases 1 to 181369)
AUTHORS     Wilson,R.K.
TITLE       Direct Submission
JOURNAL     Submitted (27-APR-2004) Genetics, Genome Sequencing Center, 4444
              Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE    4 (bases 1 to 181369)
AUTHORS     Wilson,R.K.
TITLE       Direct Submission
JOURNAL     Submitted (10-JUL-2004) Genetics, Genome Sequencing Center, 4444
              Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE    5 (bases 1 to 181369)
AUTHORS     Wilson,R.K.
TITLE       Direct Submission
JOURNAL     Submitted (18-AUG-2004) Washington University School of Medicine,
              Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
              63108, USA
              On Jul 10, 2004 this sequence version replaced gi:146576152.
COMMENT      ----- Genome Center
              Center: Washington University Genome Sequencing Center
              Web site: http://genome.wustl.edu
              Contact: submissions@watson.wustl.edu
              ----- Summary Statistics
              -----
              Center project name: C_PT011P11

NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPI-43 BAC library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Cint', Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from ResGen
(http://www.resgen.com) or Pieter de Jong and co-workers at
http://www.bacpac.chori.org.

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
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ORIGIN
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unseq
unseq

Query Match      100.0%; Score 20; DB 8; Length 181369;
Best Local Similarity 100.0%; Freq. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db  75221 TTGACCCGCCCCGTGCT 75240

RESULT 6
AC092466/c
LOCUS      216408 bp DNA linear HTG 07-SEP-2001
DEFINITION Homo sapiens chromosome UNK clone R11-606P1, WORKING DRAFT
ACCESSION AC092466
VERSION   AC092466.2 GI:15451723
KEYWORDS  HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULPTOP.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
          1 (bases 1 to 216408)
          Waterston,R.H.
          The sequence of Homo sapiens clone
          Unpublished
          2 (bases 1 to 216408)
          Waterston,R.H.
          Direct Submission
          Submitted (07-JUL-2001) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA
          On Sep 6, 2001 this sequence version replaced gi:14626400.

COMMENT      ----- Genome Center
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu/gsc/index.shtml
              ----- Project Information
              -----
              Center project name: H_NH0606P01

              ----- Summary Statistics -----
              Sequencing vector: M13; 0%
              Sequencing vector: plasmid; 97%
              Chemistry: Dye-Primer ET; 0% of reads
              Chemistry: Dye-terminator Big Dye; 97% of reads
              Assembly program: Phrap; version 0.990319
              Consensus quality: 15108 bases at least Q40
              Consensus quality: 160531 bases at least Q30
              Consensus quality: 216124 bases at least Q20
              -----
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 5 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              * 1 10000: contig of 10000 bp in length
              * 10001 10100: gap of unknown length

```



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FEATURES
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    1. 216408
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="UNK"
      /clone="RP11-606P1"
      1..10000
      /note="assembly_name:Contig1"
      10001..10100
      /estimated_length=unknown
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        10101..11588
        /note="assembly_name:Contig21"
        11589..11688
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        misc_feature
          11689..13160
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          13161..13260
          /estimated_length=unknown
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            /note="assembly_name:Contig26"
            38908..39007
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            /note="assembly_name:Contig27"

ORIGIN
  Query Match          100.0%; Score 20; DB 14; Length 216408;
  Best Local Similarity 100.0%; Pred. No. 99;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCT 20
    |||||
Db 177888 TTGACCCCGCCCTGTGCT 177869

RESULT 7
LOCUS HSA010538 331 bp DNA linear PRI 25-AUG-1998
DEFINITION Homo sapiens herg gene, exon 2 (and partial joined CDS).
ACCESSION AU010538
VERSION AU010538.1 GI:3452412
KEYWORDS cardiac specific; ether-a-go-go-related protein; herg gene;
potassium channel.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Yang, P., Paulussen, A., Verhasselt, P., Crabbe, R., Luyten, W. and
Armstrong, M.
TITLE Analysis of the human HERG gene: intron localisation and
identification of a novel inherited mutation associated with long
QT
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 331)
AUTHORS Armstrong, M.J.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1998) Armstrong M.J., Functional Genomics,
Janssen Research Foundation, 30 Turnhoutseweg, 2340, BELGIUM
FEATURES
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    1..331
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
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  /chromosome="7"
  /clone_lib="human BAC library"
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AJ010544.1:51..250,AJ010545.1:51..303,AJ010546.1:51..244,
AJ010547.1:51..150,AJ010548.1:51..323,AJ010549.1:51..237,
AJ010550.1:51..227,AJ010551.1:51..200)
  /gene="herg"
  join(51..281,AJ010539.1:51..215,AJ010540.1:51..494,
AJ010541.1:51..262,AJ010542.1:51..479,AJ010543.1:51..438,
AJ010544.1:51..250,AJ010545.1:51..303,AJ010546.1:51..244,
AJ010547.1:51..150,AJ010548.1:51..323,AJ010549.1:51..237,
AJ010550.1:51..227,AJ010551.1:51..200)
  /gene="herg"
  /function="cardiac specific potassium channel"
  /label=ERG CDS
  /product="ether-a-go-go-related protein"
  /protein_id="CA09232.1"
  /db_xref="GI:3452413"
  /db_xref="GOA:Q12809"
  /db_xref="UniProt/Swiss-Prot:Q12809"
  /translation="RRKFIANARVENCNAVITQNGFCELCGYSRAEWQRPCTDPLH
GPRTORAAQIIAAILGAEERKVEIAPYRDCSGFCLDVNVVPYKNDGANVIMFLN
FEVWEKDVMSPADDTNRKGPPTSMILPGAKTFRKLPAIIALTABSSVRSAGAG
GAGAPGAVVAVVDLTPAAPSSSLADSVTAMDVAVAGIAPAEERLALVPGSPPSA
PGOLPSPRAHSLNDPADSSCSLARTRRSCASVRRASADDIEMRAGVLPPIPRH
ASTGAMHRLRSLNSTSDSLVRYRTSKIPQILTNVVDKGPFLASPTSDREIIA
PKIKERTNVTREKTVLSGLADVLPEKLGAPRHRWTIILHSPFKAWMDLILLV
IYTVAPFVPSAAFLIKETREBGPAPTECGACQAPLAVNLIYDIWITLIINFRVTV
NANREVSHPRIRIAVHFFKWFLLDMVAIIPDLLIFSSGSEILGLIKTARILTVR
VARKIDRYSEYGAVALFLMCTFALIAWMLCIVAIQNMEOQPHMDSRIGWHLNLDQ
IKYPSNSGLGSPSIIKDKYVYALYFTFESLSLVGVGANSPTNSKIPSIQVMLIGSL
MYASIFGNVSAIIQRLYSGTARYTOMLRVEEPIRFOIIPMLRQLREYFQHAMSYT
NGIMNAVILKGPPECLADICLHNRSLLOHCKPRGATKGLRALAKFKTTHAPG
DTIVHAGDLTALYFISGSGTEILRGDVVVALIGKNDIRGRLNYARRGKSGNVRA
LTYCDLKHTRHDDLLEVDLNTPEPSDHPWSSLETFNLRDTNMLPGSGSTLEBGFPS
RQRRKLSFRRTKDKTEQGEVSALGGRGAGGSSGRPGGPGESPSGSPSPES
SEDEGPGRSSPLRLVPPSSPRPGEPGGLMBDCSKSDTCNPLSGAFSGVNIIF
SFMGVSRGROYQELPRCPAPPSLNIPLSPGRRGDSRLDALROLNRLLETRL
SADWATVQLIOLROMLTVPPAYSAVTTFGPPGTSPSLPLPSPLTFLDLSLQSPSS
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  51..281
  /gene="herg"
  /number=2

exon

ORIGIN
  Query Match          92.0%; Score 18.4; DB 8; Length 331;
  Best Local Similarity 95.0%; Pred. No. 1.2e+03;
  Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGACCCCGCCCTGTGCT 20
    |||||
Db 325 TTGACCCCGCCCTGTGCT 306

RESULT 8
LOCUS BA000030.62
WPCOMMENT
Sequence split into 91 fragments
Fragment Name Begin End
BA000030_00 1 110000
BA000030_01 100001 210000
BA000030_02 200001 310000
BA000030_03 300001 410000
BA000030_04 400001 510000
BA000030_05 500001 610000
BA000030_06 600001 710000
BA000030_07 700001 810000
BA000030_08 800001 910000
BA000030_09 900001 1010000
BA000030_10 1000001 1110000
BA000030_11 1100001 1210000
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BA000030_12 1200001 1310000
BA000030_13 1300001 1410000
BA000030_14 1400001 1510000
BA000030_15 1500001 1610000
BA000030_16 1600001 1710000
BA000030_17 1700001 1810000
BA000030_18 1800001 1910000
BA000030_19 1900001 2010000
BA000030_20 2000001 2110000
BA000030_21 2100001 2210000
BA000030_22 2200001 2310000
BA000030_23 2300001 2410000
BA000030_24 2400001 2510000
BA000030_25 2500001 2610000
BA000030_26 2600001 2710000
BA000030_27 2700001 2810000
BA000030_28 2800001 2910000
BA000030_29 2900001 3010000
BA000030_30 3000001 3110000
BA000030_31 3100001 3210000
BA000030_32 3200001 3310000
BA000030_33 3300001 3410000
BA000030_34 3400001 3510000
BA000030_35 3500001 3610000
BA000030_36 3600001 3710000
BA000030_37 3700001 3810000
BA000030_38 3800001 3910000
BA000030_39 3900001 4010000
BA000030_40 4000001 4110000
BA000030_41 4100001 4210000
BA000030_42 4200001 4310000
BA000030_43 4300001 4410000
BA000030_44 4400001 4510000
BA000030_45 4500001 4610000
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BA000030_67 6700001 6810000
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BA000030_70 7000001 7110000
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BA000030_76 7600001 7710000
BA000030_77 7700001 7810000
BA000030_78 7800001 7910000
BA000030_79 7900001 8010000
BA000030_80 8000001 8110000
BA000030_81 8100001 8210000
BA000030_82 8200001 8310000
BA000030_83 8300001 8410000
BA000030_84 8400001 8510000

BA000030_85 8500001 8610000
BA000030_86 8600001 8710000
BA000030_87 8700001 8810000
BA000030_88 8800001 8910000
BA000030_89 8900001 9010000
BA000030_90 9000001 9100000
Continuation (63 of 91) of BA000030 from base 6200001 (BA000030 Streptomyces avermitilis)

Query Match 87.0%; Score 17.4; DB 1; Length 110000;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGACCCCGCCCTGTGTCG 19
DB 88490 TTCAACCCCGCCCTGTGTCG 88508

RESULT 9
AC150790_1/c
WPCOMMENT
Sequence split into 6 fragments LOCUS AC150790 Accession AC150790
Fragment Name Begin End
AC150790_0 1 110000
AC150790_1 100001 210000
AC150790_2 200001 310000
AC150790_3 300001 410000
AC150790_4 400001 510000
AC150790_5 500001 543768
Continuation (2 of 6) of AC150790 from base 100001 (AC150790 Bos taurus clone CH240-469N)

Query Match 87.0%; Score 17.4; DB 14; Length 110000;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGTGTCG 20
DB 17184 TGACCCCGCCCTGTGTCG 17166

RESULT 10
AC140158/c
LOCUS AC140158 155060 bp DNA linear HTG 03-APR-2003
DEFINITION Felis catus clone RP86-578M14, WORKING DRAFT SEQUENCE, 18 ordered
pieces.
ACCESSION AC140158
VERSION AC140158.2 GI:29501862
KEYWORDS HTG: HTGS PHASE2; HTGS_DRAFT.
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
REFERENCE 1 (bases 1 to 155060)
AUTHORS Akhter, N., Antonellis, A., Ayale, K., Beckstrom-Sternberg, S. M.,
Benjamin, B., Blakesley, R. W., Bouffard, G. G., Brinkley, C., Brooks, S.,
Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idoi, J. R., Karlins, E.,
Laric, P., Lee-Ihn, S.-O., Legaspi, R., Maduro, Q. L., Maduro, V. B.,
Margulies, E. H., Mastello, C., Markert, B., McDowell, J.,
Pegutigan, C., Pearson, R., Portnoy, M. E., Prasad, A.,
Reddi-Dugue, N., Schandler, K., Schuler, M. G., Sison, C.,
Stentrop, S., Thomas, J. W., Thomas, P. J., Touchman, J. W., Vogt, J. L.,
Weberby, K. D., Wiggins, L., Young, A., and Green, E. D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 155060)
REFERENCE
AUTHORS Green, E. D.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2003) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 155060)
AUTHORS Green, E. D.
TITLE Direct Submission

JOURNAL
Submitted (03-APR-2003) NIH Intramural Sequencing Center, 8717
Grovermont Circle, Gaithersburg, MD 20877, USA
On Apr 3, 2003 this sequence version replaced g1:28467153.

COMMENT

Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov

Project Information
Center project name: dzg
Center clone name: 578M14

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152104 bases at least Q40
Consensus quality: 152758 bases at least Q30
Consensus quality: 153143 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 153360; sum-of-contigs
Quality coverage: 11.84x in Q20 bases; agarose-fp
Quality coverage: 12.36x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 8363: contig of 8363 bp in length
* 8364 8463: gap of unknown length
* 8464 12801: contig of 4338 bp in length
* 12802 12901: gap of unknown length
* 12902 15263: contig of 2362 bp in length
* 15264 15363: gap of unknown length
* 15364 25824: contig of 10461 bp in length
* 25825 25825: gap of unknown length
* 25925 38785: contig of 12861 bp in length
* 38786 38885: gap of unknown length
* 38886 50988: contig of 12003 bp in length
* 50989 59181: contig of 8193 bp in length
* 59182 59281: gap of unknown length
* 59282 75321: contig of 16040 bp in length
* 75322 75421: gap of unknown length
* 75422 81307: contig of 5886 bp in length
* 81308 81407: gap of unknown length
* 81408 101800: contig of 20393 bp in length
* 101801 101900: gap of unknown length
* 101901 108688: contig of 6788 bp in length
* 108689 108788: gap of unknown length
* 108789 115255: contig of 6467 bp in length
* 115256 115355: gap of unknown length
* 115356 117889: contig of 2534 bp in length
* 117890 117989: gap of unknown length
* 117990 12675: contig of 466 bp in length
* 122676 122775: gap of unknown length

FEATURES

source

* 122776 125902: contig of 3127 bp in length
* 125903 126002: gap of unknown length
* 126003 141550: contig of 15548 bp in length
* 141551 141650: gap of unknown length
* 141651 144316: contig of 2666 bp in length
* 144317 144416: gap of unknown length
* 144417 15060: contig of 10644 bp in length.
Location/Qualifiers

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/mol_type="genomic DNA"
/db_xref="taxon:9685"
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/clone_11b="RP86"
1..132448
/note="clone overlaps with Genbank Accession Number
AC135221 clone RP86-567F9 (center project name dzf)"

misc_feature

1..8363
/note="assembly_fragment"

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vector_side:left"
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12802..12901
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25925..38785
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38786..38885
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38886..50888
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50989..59181
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misc_feature

59182..59281
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59282..75321
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75322..75421
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75422..81307
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misc_feature

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misc_feature

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misc_feature

117990..12675
/note="assembly_fragment"


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                    22793..156383
                    /note="clone overlap with GenBank Accession Number
                    AC140158 clone RP86-578M14 (center project name dzg)"
gap               35504..35603
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                    35604..75477
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                    75478..75577
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                    75578..83833
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                    83834..83933
                    /estimated_length=unknown
                    83934..100101
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                    100202..103529
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                    126421..141405
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misc_feature      /note="assembly_fragment"
                    146217..146316
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misc_feature      /note="assembly_fragment
                    clone_end:SP6
                    vector_side:right"

ORIGIN
Query Match      87.0%; Score 17.4; DB 14; Length 156383;
Best Local Similarity 94.7%; Pred.No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 TGACCCGCGCCCTGCTGCT 20
Db      47216 TGACCCGCGCCCTGCTGCT 47198

RESULT 12
AC157414/c      212682 bp      DNA      linear      HTG 01-JUL-2005
LOCUS          unordered pieces.
DEFINITION     Bos taurus clone CH240-66017, *** SEQUENCING IN PROGRESS ***, 22
ACCESSION     AC157414
VERSION      AC157414.2 GI:68302799
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE       Bos taurus (cow)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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REFERENCE
AUTHORS
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 212682)
Allen,C., Allen,H., Albrooks,S., Amlin,A., Angiano,D.,
Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Blewailo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., p'Souza,L.,
Dayila,M.L., Davis,C., Davy-Carroll,L., De Ande,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Din,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durkin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gedregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Huliy,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Louissege,H., Lozada,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Mallory,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenan,E.,
Milosavljevic,A., Miner,G., Minje,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwokoleheneh,O., Okwomou,G., Olarunmugbon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,J., Pfankoch,C.,
Plopper,F., Polindexter,A., Popovic,D., Primus,E., Pu,L.,-P.,
Puazo,M., Quiroz,J., Rachlin,B., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojars,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Saverly,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajd,D.,
Sneid,A., Sodergren,E., Song,X.-Z., Sorella,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Svatek,A., Taboc,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejo,J., Umani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 212682)
Mortley,K.C.
Direct Submission
Submitted (16-FEB-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 212682)
Cow Genome Sequencing Consortium.
Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 29, 2005 this sequence version replaced gi:59658648.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated

```

by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: PDV
Center clone name: CH240-66017
----- Summary Statistics

Assembly program: Atlas 3.0;
Consensus quality: 205518 bases at least Q40
Consensus quality: 206814 bases at least Q30
Estimated insert size: 209965; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1      8799: contig of 8799 bp in length
      8800      8849: gap of 50 bp
      8850      1169: contig of 2770 bp in length
      11670      15412: contig of 3743 bp in length
      15463      17502: contig of 2040 bp in length
      17503      17685: gap of 183 bp
      17686      19548: contig of 1863 bp in length
      19549      19648: gap of unknown length
      19649      23412: contig of 3764 bp in length
      23413      23566: gap of 154 bp
      23567      59114: contig of 35548 bp in length
      59115      59164: gap of 50 bp
      59165      64345: contig of 5181 bp in length
      64346      64395: gap of 50 bp
      64396      79925: contig of 15530 bp in length
      79926      79975: gap of 50 bp
      79976      101261: contig of 21286 bp in length
      101262      101311: gap of 50 bp
      101312      106833: contig of 5522 bp in length
      106834      107126: gap of 293 bp in length
      107127      115309: contig of 8183 bp in length
      115310      115727: gap of 418 bp
      115728      117869: contig of 2142 bp in length
      117870      118409: gap of 540 bp
      118410      133361: contig of 14952 bp in length
      133362      133411: gap of 50 bp
      133412      136965: contig of 23554 bp in length
      136966      157015: gap of 50 bp
      157016      166550: contig of 9535 bp in length
      166551      167100: gap of 550 bp
      167101      168570: contig of 1470 bp in length
      168571      168670: gap of unknown length
      168671      172341: contig of 3671 bp in length
      172342      172391: gap of 50 bp
      172392      174828: contig of 2437 bp in length
      174829      174879: gap of 50 bp
      174879      178654: contig of 3776 bp in length
      178655      178704: gap of 50 bp
      178704      211552: contig of 32848 bp in length

```

FEATURES

* 211553 211652: gap of unknown length
* 211653 212682: contig of 1030 bp in length.
Location/Qualifiers
1. .212682

source
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-66017"

gap
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/estimated_length=50

gap
11620. .11669
/estimated_length=50

gap
15413. .15462
/estimated_length=50

gap
17503. .17685
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gap
19549. .19648
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gap
23413. .23566
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gap
59115. .59164
/estimated_length=50

gap
64346. .64395
/estimated_length=50

gap
79926. .79975
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gap
101262. .101311
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106834. .107126
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115310. .115727
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gap
117870. .118409
/estimated_length=540

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133362. .133411
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168571. .168670
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172342. .172391
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gap
174829. .174879

gap
178654. .178704

gap
211552. .211652

gap
212682. .212682

gap
212682. .212682

gap
212682. .212682

gap
212682. .212682

Query Match 87.0%; Score 17.4; DB 14; Length 212682;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGACCCCGCCCTGTCGT 20
DB 77938 TGACCCCGCCCTGTCGT 77920
RESULT 13
AC150564/c
LOCUS
DEFINITION Bos taurus clone CH240-115C4, WORKING DRAFT SEQUENCE, 4 ordered
pieces.
ACCESSION AC150564
VERSION AC150564.3 GI:51468287
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 218381)
Muzny, D., Metzker, M., Adams, C., Agbai II, O., Allen, C.,
Albrooks, S., Archer, P., Arredondo, H., Bandaranatke, D., Bangura, L.,
Beltran, B., Beltran, R., Beraducci, A., Biswal, K., Blyth, P.,
Bonham, H., Buhay, C., Burch, P., Cadoree, I., Canada, A., Cardenas, V.,

Carter, K., Cavazos, I., Chacko, J., Chahour, M., Chavez, D., Chen, A., Chen, G., Chen, R., Cheng, M.-T., Chu, J., Clerc, K., Cockrell, R., Coyle, M., Cree, A., Curry, S., Dai, W., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Delgado, O., Denison, S., Derano, C., Ding, Y., Dinh, H., Donlin, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Durbin, K., Daluda, D., Egan, A., Escoto, M., Espinosa, V., Eugene, C., Fa, M., Fernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P., Fowler, G., Fu, Q., Fuh, E., Garcia, A., Garcia, R., Garner, T., Gaikin, C., Ganch, S., Ghouse, S., Gili, R., Gonzalez, D., Gonzalez-Garay, M., Guevara, W., Holder, M., Haland, W., Habberlen, K., Hall, B., Hamid, H., Hamilton, K., Harbes, B., Harris, R., Haylak, P., Haves, A., Hawkins, B., Hayes, S., Hemphill, L., Hernandez, J., Hines, S., Hitchens, M., Hodgson, A., Hognes, M., Hollins, B., Howell, L. T., Hulyk, S., Hume, J., Ito, K., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kafafus, K., Kelly, S., Keys, T., Khan, Z., King, L., Kovar, C., Kowis, A., Kowis, C., Lara, F., Leal, S., Lee, K., Lee, S., Legall, P. I., Lemon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linneil, W., Liu, W., Liu, Y.-S., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuhewa, L., Lozardo, R., Luk, T., Madu, R., Maleshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, E., McEljeland, H., McPherson, J., Mercadao, C., Milosavljevic, A., Milija, E., Morgan, M., Morris, S., Mundaas, M., Murray, D., Narath, L., Ngo, D., Nguyen, N., Norwig-Baerth, E., Not, A., Nwokenemeh, O., Obregon, M., Ochi-Okorie, C., Odeh, E., Okwom, G., Okwom, K., Parker, D., Pasternak, S., Patel, B., Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Primus, E., Pu, L.-L., Puzo, M., Qin, X., Quinn, A., Quiroz, J., Rabata, D., Rachlin, E., Reigh, R., Ren, Y., Reuter, M., Richards, S., Rives, C., Rodriguez, F., Rojas, A., Ruiz, S. J., Sana, M., Sanders, W., Santibanez, J., Santos, R., Saver, G., Scherer, S., Shen, H., Shen, Y., Sisson, I., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Syatek, A., Taylor, B., Taylor, T., Thomas, N., Thorn, R., Thornton, R., Trejos, Z., Usmani, K., Vargio, C., Verdusco, D., Villasana, D., Virk, D., Volkov, A., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Wei, X., Wheeler, D., Williams, G., Williams, R., Worley, K., Wright, R., Wu, J., Yan, S., Yan, K., Yau, Y., Yu, F., Zhang, J., Zhang, L., Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 218381)
Worley, K. C.

Direct Submission
Submitted (27-JUL-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 218381)
Worley, K. C.

Direct Submission
Submitted (21-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 20, 2004 this sequence version replaced gi:50726741.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help.tmc.edu

----- Project Information
Center project name: FBRI
Center clone name: CH240-115C4
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 217685 bases at least Q40
Consensus quality: 217796 bases at least Q30
Consensus quality: 217855 bases at least Q20
Estimated insert size: 224869; sum-of-contrigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/denbank_drfc_data.html)
* The sequence data in this record represents an 'enhanced' version

* of a Phase 2 submission. The indicated order and orientation of
* each sequence has been established using one or more of the
* following: read-pair data from individual subclones, overlaps
* with neighboring clones, alignment with available reference
* sequence (e.g., human), and/or confirmation by PCR testing.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 37410: contig of 37410 bp in length
* 37411 37910: gap of 500 bp
* 37411 167201: contig of 129291 bp in length
* 167202 167551: gap of 350 bp
* 167552 187282: contig of 19731 bp in length
* 187283 187482: gap of 200 bp
* 187483 218381: contig of 30899 bp in length.

FEATURES
source
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/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-115C4"
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37911. 167201
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167202. 167551
/note="assembly_name:gap"
167202. 167551
/estimated_length=350
167552. 187282
/note="assembly_name:Contig20"
187283. 187482
/note="assembly_name:gap"
187283. 187482
/estimated_length=200
187483. 218381
/note="assembly_name:Contig21"

ORIGIN
Query Match 87.0%; Score 17.4; DB 14; Length 218381;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGACCCCGCCCTGTCGT 20
Db 112566 TGACCCCGCCCTGTCGT 112548

RESULT 14
AC098101/c 243300 bp DNA linear HTG 10-MAY-2003
LOCUS
DEFINITION Rattus norvegicus clone CH230-82p23, WORKING DRAFT SEQUENCE, 3
unordred pieces.
ACCESSION AC098101
VERSION AC098101.6 GI:30520383
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 243300)
Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D., Anyalbech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandenaike, D., Barber, M., Barnstead, M., Barnstead, F., Blawie, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bubay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Fails, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Geisberg, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, J., Havlek, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Huliy, S., Hume, J., Idledit, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapachy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Louiseged, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokelimeh, O., Okwou, G., Olarnunagoon, A., Pal, S., Parke, K., Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primm, E., Pu, L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Reiter, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajic, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabors, Z., Umant, K., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Tjorja, Z., Uman, K., Valas, R., Vera, V., Villanueva, D., Walgren, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausen, A., Weise, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G., and Gibbs, R. A.

TITLE Direct Submission

Unpublished

2 (bases 1 to 243300)

Worley, K. C.

REFERENCES Direct Submission

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 243300)

Rat Genome Sequencing Consortium.

REFERENCES Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCES TITLE

JOURNAL

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/atlantis/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GGHF

Center clone name: CH230-82P23

----- Summary Statistics
Assembly program: Atlas 3.0;

Consensus quality: 217745 bases at least Q40

Consensus quality: 224557 bases at least Q30

Estimated insert size: 232921; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 240318: contig of 240318 bp in length

* 240319 240418: gap of unknown length

* 240419 241639: contig of 1221 bp in length

* 241640 241739: gap of unknown length

* 241740 243300: contig of 1561 bp in length.

Location/Qualifiers

1..243300

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-82P23"

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misc_feature

236801..240318

misc_feature

240319..240418

gap

240419..241639

gap

241640..241739

gap

----- Query Match
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

----- Db
1 TTGACCCGCGCCGTCG 19

152387 TTGACCCGCGCCGTCG 152369

----- RESULT 15
AC150514

AC150514

DEFINITION

Bos taurus clone CH240-109B14, WORKING DRAFT SEQUENCE, 3 ordered

pieces.

AC150514 6 GI:51468284

KEYWORDS

HTG, HTGS_PHASE2, HTGS_DRAFT, HTGS_FULFILL.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Bovidae; Bovinae; Bos.

1 (bases 1 to 246115)

Muzny, D., Metzger, M., Adams, C., Agbai II, O., Allen, C.,

Albrooke, S., Archer, P., Arredondo, H., Bandaranaike, D., Bangura, L., Beltran, B., Beltran, R., Berarducci, A., Biswal, K., Blyth, P., Bonham, K., Bunay, C., Burch, P., Cadore, I., Canada, A., Cardenas, V., Carter, K., Cavazos, I., Chacko, J., Chahrour, M., Chavez, D., Chen, A., Chen, G., Chen, R., Cheng, M.-T., Chu, J., Clerc, K., Cockrell, R., Coyle, M., Cree, A., Curry, S., Dai, W., Davila, M.L., Davis, C., Day-Carroll, L., De Anda, C., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Donlin, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Durbin, K., Dziuda, D., Egan, A., Escotto, M., Espinosa, V., Eugene, C., Fa, M., Fernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P., Fowler, G., Fu, Q., Fuh, E., Garcia, A., Garcia, R., Garner, T., Galetin, C., Gench, S., Ghose, S., Gill, R., Gonzalez, D., Gonzalez-Garay, M., Guevara, W., Holder, M., Haaland, M., Haebler, K., Hall, B., Hamid, H., Hamilton, K., Harbes, B., Harris, R., Havlak, P., Hawes, A., Hawkins, E., Hayes, S., Hemphill, L., Hernandez, J., Hines, S., Hitchens, M., Hodgson, A., Hogue, M., Hollins, B., Howell, L.T., Hulik, S., Hume, J., Imo, K., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kalafus, K., Kelly, S., Keys, T., Khan, Z., King, L., Koyar, C., Kowals, A., Kowals, C., Lara, F., Leal, S., Lee, K., Lee, S., Legall, F.I., Lemon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linell, M., Liu, W., Liu, Y.-S., Liu, Y., Llyanage, D., London, P., Lopez, J., Lorensheva, L., Lozano, R., Luk, T., Madu, R., Maheshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, E., McCelland, H., McPherson, J., Mercadeo, C., Milosavljevic, A., Milija, E., Morgan, M., Morris, S., Munidasa, M., Murray, D., Nazareth, L., Ngo, D., Nguyen, N., Norwig-Bastlaugh, E., Not, A., Nwankwelu, O., Obregon, M., Ochi-Okorie, C., Odeh, E., Okunolu, G., Okunolu, K., Parker, D., Pasternak, S., Patel, B., Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Primus, B., Pu, L.-L., Puzo, M., Qin, X., Quinn, A., Quiroz, J., Rabata, D., Rachlin, E., Reigh, R., Ren, Y., Reuter, M., Richards, S., Rives, C., Rodriguez, F., Rojas, A., Ruiz, S.J., Sana, M., Sanders, W., Santibanez, J., Santos, R., Savary, G., Scherer, S., Shen, H., Shen, Y., Sieson, I., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Swatek, A., Taylor, E., Taylor, T., Thomas, N., Thorm, R., Thornton, R., Trejos, Z., Usmani, K., Valgo, C., Verduzco, D., Villalana, D., Virk, D., Volkov, A., Walder, L., Walker, B., Wang, Q., Wang, S., Warren, J., Wei, X., Wheeler, D., Williams, G., Williams, R., Worley, K., Wright, R., Wu, J., Yakub, S., Yan, K., Yau, Y., Yu, F., Zhang, J., Zhang, L., Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.

Unpublished
2 (bases 1 to 236115)
Worley, K.C.
Direct Submission
Submitted (24-JUN-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 236115)
Worley, K.C.
Direct Submission
Submitted (21-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 20, 2004 this sequence version replaced gi:5083862.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help.tmc.edu
----- Project Information
Center project name: FERO
Center clone name: CH240-109B14
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 23518 bases at least Q40
Consensus quality: 23560 bases at least Q30
Consensus quality: 23513 bases at least Q20
Estimated insert size: 251101; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone
* The sequence data in this record represents an 'enhanced' version
* of a Phase 2 submission. The indicated order and orientation of
* each sequence has been established using one or more of the
* following: read-pair data from individual subclones, overlaps
* with neighboring clones, alignment with available reference
* sequence (e.g., human), and/or confirmation by PCR testing.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 29106: contig of 29106 bp in length
* 29107 29606: gap of 500 bp
* 29607 157023: contig of 127417 bp in length
* 157024 157043: gap of 20 bp
* 157044 236115: contig of 79072 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-109B14"
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29107..29606
/note="assembly_name:gap"
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29607..157023
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157024..157043
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157044..236115
/note="assembly_name:Contig44"

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Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACCCCGCCCTGCTG 18
|||||
DB 71982 TGACCCCGCCCTGCTG 71998

Search completed: April 10, 2006, 16:19:54
Job time : 1134.5 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 10, 2006, 15:06:53 ; Search time 311.5 Seconds
(without alignments)
256.858 Million cell updates/sec

Title: US-10-696-708A-60

Perfect score: 1 ggtccgcgcgcgcactct 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New.*
1: /SID5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SID5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SID5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SID5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SID5/ptodata/2/pubpna/US05_NEW_PUB.seq:*
6: /SID5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
7: /SID5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SID5/ptodata/2/pubpna/US10_NEW_PUB.seq1.*
9: /SID5/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
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14: /SID5/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
15: /SID5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.8	84.0	1698	US-10-750-185-49068	Sequence 49068, A
2	16.8	84.0	1698	US-10-750-623-49068	Sequence 49068, A
3	16.8	84.0	2136	US-10-453-372-999	Sequence 999, App
4	16.8	84.0	2153	US-10-453-372-997	Sequence 997, App
5	16.8	84.0	15660	US-10-453-372-1003	Sequence 1003, App
6	16.8	84.0	15660	US-10-453-372-1001	Sequence 1001, App
7	16.8	84.0	18209	US-11-065-695-19	Sequence 19, App1
8	16.8	84.0	635	US-10-301-480-56398	Sequence 56398, A
9	16.8	84.0	635	US-10-301-480-1176807	Sequence 1176807, A
10	15.2	76.0	924	US-10-932-182A-2199	Sequence 2199, App
11	15.2	76.0	924	US-10-932-182A-2199	Sequence 2199, App
12	15.2	76.0	974	US-10-301-480-571148	Sequence 571148, A
13	15.2	76.0	974	US-10-301-480-1184557	Sequence 1184557, A
14	15.2	76.0	1807	US-11-132-329-125	Sequence 125, App
15	15.2	76.0	1694969	US-10-506-454-1690	Sequence 1690, App
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17	14.8	74.0	201	US-10-995-561-21548	Sequence 21548, A
18	14.8	74.0	201	US-10-995-561-71091	Sequence 71091, A

19	14.8	74.0	201	US-10-995-561-71202	Sequence 71202, A
20	14.8	74.0	387	US-09-925-065A-483357	Sequence 483357, A
21	14.8	74.0	547	US-09-925-065A-107498	Sequence 107498, A
22	14.8	74.0	550	US-09-925-065A-473524	Sequence 473524, A
23	14.8	74.0	550	US-09-925-065A-473525	Sequence 473525, A
24	14.8	74.0	565	US-09-925-065A-930079	Sequence 930079, A
25	14.8	74.0	565	US-09-925-065A-950510	Sequence 950510, A
26	14.8	74.0	567	US-09-925-065A-923657	Sequence 923657, A
27	14.8	74.0	567	US-09-925-065A-947533	Sequence 947533, A
28	14.8	74.0	572	US-10-301-480-207355	Sequence 207355, A
29	14.8	74.0	572	US-10-301-480-820764	Sequence 820764, A
30	14.8	74.0	626	US-09-925-065A-813651	Sequence 813651, A
31	14.8	74.0	18540	US-10-995-561-13223	Sequence 13223, A
32	14.8	74.0	20773	US-10-995-561-13222	Sequence 13222, A
33	14.8	74.0	403278	US-10-995-561-13421	Sequence 13421, A
34	14.4	72.0	25	US-10-933-982-61618	Sequence 61618, A
35	14.4	72.0	73102	US-10-330-773-865	Sequence 865, App
36	14.2	71.0	25	US-11-121-849-103670	Sequence 103670, A
37	14.2	71.0	70	US-10-310-914A-9462	Sequence 9462, App
38	14.2	71.0	201	US-10-995-561-12032	Sequence 12032, A
39	14.2	71.0	201	US-10-995-561-12068	Sequence 12068, A
40	14.2	71.0	201	US-10-995-561-12106	Sequence 12106, A
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42	14.2	71.0	473	US-09-925-065A-794348	Sequence 794348, A
43	14.2	71.0	473	US-09-925-065A-802285	Sequence 802285, A
44	14.2	71.0	478	US-09-925-065A-470449	Sequence 470449, A
45	14.2	71.0	499	US-10-349-331-394	Sequence 394, App

ALIGNMENTS

RESULT 1
US-10-750-185-49068
Sequence 49068, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: NM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49068
LENGTH: 1698
TYPE: DNA
ORGANISM: Bovine 19866881515255
US-10-750-185-49068

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QY 1 GGTCCGTCAGGCGACTCT 20
DB 509 GGTCCGTCAGGCGACTCT 528

RESULT 2
US-10-750-623-49068
Sequence 49068, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49068
LENGTH: 1698
TYPE: DNA
ORGANISM: Bovine 19866881515255
US-10-750-623-49068

Query Match 84.0%; Score 16.8; DB 8; Length 1698;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 509 GGTCCGTCACGCGCACTCT 528

RESULT 3
US-10-453-372-999
Sequence 999, Application US/10453372
Publication No. US2006000323A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-589 A

CURRENT APPLICATION NUMBER: US/10/453,372

CURRENT FILING DATE: 2003-06-03

PRIOR APPLICATION NUMBER: 09/789990

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 60/185967

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 09/823187

PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/195792

PRIOR FILING DATE: 2000-03-10

PRIOR APPLICATION NUMBER: 09/839446

PRIOR FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/199476

PRIOR FILING DATE: 2000-03-25

PRIOR APPLICATION NUMBER: 09/939398

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/227800

PRIOR FILING DATE: 2000-08-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1609

SOFTWARE: Curaseqlist version 0.1

SEQ ID NO 999

LENGTH: 2136

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(2136)

US-10-453-372-999

Query Match 84.0%; Score 16.8; DB 8; Length 2136;
Best Local Similarity 90.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1259 GGTCCGTCACGCGCACTCT 1278

RESULT 4
US-10-453-372-997

Sequence 997, Application US/10453372

Publication No. US2006000323A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-589 A

CURRENT APPLICATION NUMBER: US/10/453,372

CURRENT FILING DATE: 2003-06-03

PRIOR APPLICATION NUMBER: 09/789390

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 60/185967

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 09/823187

PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/195792

PRIOR FILING DATE: 2000-03-10

PRIOR APPLICATION NUMBER: 09/839446

PRIOR FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/199476

PRIOR FILING DATE: 2000-03-25

PRIOR APPLICATION NUMBER: 09/863776

PRIOR FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: 60/208263

PRIOR FILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: 09/939398

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/227800

PRIOR FILING DATE: 2000-08-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1609

SOFTWARE: Curaseqlist version 0.1

SEQ ID NO 997

LENGTH: 2153

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (16)..(2136)

US-10-453-372-997

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Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1265 GGTCCGTCACGCGCACTCT 1284

RESULT 5
US-10-453-372-1003

Sequence 1003, Application US/10453372

Publication No. US2006000323A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-589 A

CURRENT APPLICATION NUMBER: US/10/453,372

CURRENT FILING DATE: 2003-06-03

PRIOR APPLICATION NUMBER: 09/789390

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 60/185967

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 09/823187

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;; PRIOR FILING DATE: 2001-03-29
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;; PRIOR APPLICATION NUMBER: 09/839446
;; PRIOR FILING DATE: 2001-03-19
;; PRIOR APPLICATION NUMBER: 60/199476
;; PRIOR FILING DATE: 2000-03-25
;; PRIOR APPLICATION NUMBER: 09/863776
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: 60/208263
;; PRIOR FILING DATE: 2000-05-31
;; PRIOR APPLICATION NUMBER: 09/939398
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: Cirsaseq1 version 0.1
;; SEQ ID NO 1003
;; LENGTH: 6343
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (105)..(5810)
US-10-453-372-1003
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Best Local Similarity 90.0%; Pred. No. 24;
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Oy      1 GGTCCCGTCACGCGCACTCT 20
Db      2674 GGTCCCGTCACGCGCACTCT 2693
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RESULT 6

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US-10-453-372-1001
; Sequence 1001, Application US/10453372
; Publication No. US2006000323A1
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GENERAL INFORMATION:

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;; APPLICANT: Alsbetook, et al.
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-589 A
;; CURRENT APPLICATION NUMBER: US/10/453,372
;; PRIOR FILING DATE: 2003-06-03
;; PRIOR APPLICATION NUMBER: 09/789390
;; PRIOR FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/823187
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195792
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: 09/839446
;; PRIOR FILING DATE: 2001-03-19
;; PRIOR APPLICATION NUMBER: 60/199476
;; PRIOR FILING DATE: 2000-03-25
;; PRIOR APPLICATION NUMBER: 09/863776
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: 60/208263
;; PRIOR FILING DATE: 2000-05-31
;; PRIOR APPLICATION NUMBER: 09/939398
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: Cirsaseq1 version 0.1
;; SEQ ID NO 1001
;; LENGTH: 15660
;; TYPE: DNA
;; ORGANISM: Homo sapiens
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;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1649)..(15133)
US-10-453-372-1001
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Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db      11646 GGTCCCGTCACGCGCACTCT 11665
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RESULT 7

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US-11-065-695-19
; Sequence 19, Application US/11065695
; Publication No. US20060024688A1
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GENERAL INFORMATION:

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;; APPLICANT: STONE, EDWIN
;; TITLE OF INVENTION: ALTERATIONS OF FIBULIN GENES IN MACULAR DEGENERATION
;; FILE REFERENCE: IOWA:058US
;; CURRENT APPLICATION NUMBER: US/11/065,695
;; PRIOR FILING DATE: 2005-02-24
;; PRIOR APPLICATION NUMBER: 60/547,216
;; PRIOR FILING DATE: 2004-02-24
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;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 19
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;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1230)..(17140)
US-11-065-695-19
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Db      13650 GGTCCCGTCACGCGCACTCT 13669
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RESULT 8

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US-10-301-480-563398
; Sequence 563398, Application US/10301480
; Publication No. US20060057564A1
```

GENERAL INFORMATION:

```
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
;; FILE REFERENCE: 108827.137
;; CURRENT APPLICATION NUMBER: US/10/301,480
;; PRIOR FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US 10/215,598
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: US 60/311,695
;; PRIOR FILING DATE: 2001-08-10
;; NUMBER OF SEQ ID NOS: 122618
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 563398
;; LENGTH: 635
;; TYPE: DNA
;; ORGANISM: Homo sapien
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FEATURE:

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;; NAME/KEY: misc feature
;; LOCATION: 439..501, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513,
;; LOCATION: 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525,
;; LOCATION: 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537,
;; LOCATION: 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548
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; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560,
; LOCATION: 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572,
; LOCATION: 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584,
; LOCATION: 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 596, 597, 598, 599, 600, 601, 602, 603
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1176807

Query Match          80.0%; Score 16; DB 10; Length 635;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CCGTCACGCGCACTCT 20
        |||||
Db      317 CCGTCACGCGCACTCT 332

RESULT 9
US-10-301-480-1176807
; Sequence 1176807, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1176807
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 439, 501, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513,
; LOCATION: 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525,
; LOCATION: 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537,
; LOCATION: 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560,
; LOCATION: 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572,
; LOCATION: 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584,
; LOCATION: 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 596, 597, 598, 599, 600, 601, 602, 603
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1176807

Query Match          80.0%; Score 16; DB 10; Length 635;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CCGTCACGCGCACTCT 20
        |||||
Db      317 CCGTCACGCGCACTCT 332

RESULT 10
US-10-932-182A-2199/c
; Sequence 2199, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2199
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2199

Query Match          76.0%; Score 15.2; DB 9; Length 924;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGTCCGTCACGCGCACTCT 20
        |||||
Db      146 GGTCCATCACGCGGCGCTCT 127

RESULT 11
US-10-932-182A-2199/c
; Sequence 2199, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2199
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2199

Query Match          76.0%; Score 15.2; DB 9; Length 924;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGTCCGTCACGCGCACTCT 20
        |||||
Db      146 GGTCCATCACGCGGCGCTCT 127

RESULT 12
US-10-301-480-571148/c
; Sequence 571148, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
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```

; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571148
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-571148

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```

Query Match          76.0%; Score 15.2; DB 10; Length 974;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 GGTCCCGTCACGCGCACTCT 20
      ||||| ||||| ||||| |||||
Db      109 GGTCCCGGAGCTGCACTCT 90

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RESULT 13
US-10-301-480-1184557/c
; Sequence 1184557, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1184557
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1184557

```

```

Query Match          76.0%; Score 15.2; DB 10; Length 974;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

Qy      1 GGTCCCGTCACGCGCACTCT 20
      ||||| ||||| ||||| |||||
Db      109 GGTCCCGGAGCTGCACTCT 90

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RESULT 14
US-11-122-329-125/c
; Sequence 125, Application US/11122329
; Publication No. US20060019272A1
; GENERAL INFORMATION:
; APPLICANT: Geraci, Mark
; APPLICANT: Bull, Todd
; APPLICANT: Voelkel, Norbert
; APPLICANT: Coldren, Chris
; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
; FILE REFERENCE: 2848-54
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US/11/122,329
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 1807

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-122-329-125

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Query Match          76.0%; Score 15.2; DB 14; Length 1807;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 GGTCCCGTCACGCGCACTCT 20
      ||||| ||||| ||||| |||||
Db      381 GGTCCCGTCACGCGCACTCT 362

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RESULT 15
US-10-506-454-1690/c
; Sequence 1690, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhnevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozlyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; FILE REFERENCE: FID001
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1690
; LENGTH: 1694969
; TYPE: DNA
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1690

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Query Match          76.0%; Score 15.2; DB 7; Length 1694969;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 GGTCCCGTCACGCGCACTCT 20
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Db      303067 GGTCCCGTCGAGCAGCGCT 303048

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Job time : 313.5 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 15:06:00 ; Search time 442 Seconds
(without alignments)
374.180 Million cell updates/sec

Title: US-10-696-708A-60
Perfect score: 20
Sequence: 1 ggtccgcgcacgcgacctc 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications_NA_Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-09-735-995-60	Sequence 60, Appl
2	20	100.0	20	US-10-696-708-60	Sequence 60, Appl
3	16.8	84.0	29	US-10-934-998-252	Sequence 252, App
4	16.8	84.0	201	US-10-719-993-6589	Sequence 6589, App
5	16.8	84.0	201	US-10-719-993-6593	Sequence 6593, App
6	16.8	84.0	201	US-10-719-993-41420	Sequence 41420, A
7	16.8	84.0	201	US-10-719-993-41474	Sequence 41474, A
8	16.8	84.0	564	US-10-934-998-131	Sequence 131, App
9	16.8	84.0	1851	US-10-425-115-87910	Sequence 87910, A
10	16.8	84.0	2153	US-10-138-588-17	Sequence 17, Appl
11	16.8	84.0	3407	US-09-814-353-21856	Sequence 21856, A
12	16.8	84.0	3729	US-10-719-993-416	Sequence 416, App
13	16.8	84.0	3910	US-10-450-763-3924	Sequence 3924, App
14	16.8	84.0	4073	US-10-019-065A-34	Sequence 34, Appl
15	16.8	84.0	5935	US-10-115-479-87	Sequence 87, Appl
16	16.8	84.0	6024	US-10-934-998-177	Sequence 87, Appl
17	16.8	84.0	6343	US-10-114-153-87	Sequence 87, Appl
18	16.8	84.0	8243	US-10-114-153-85	Sequence 85, Appl
19	16.8	84.0	8546	US-10-934-998-52	Sequence 52, Appl
20	16.8	84.0	12381	US-11-049-637-3	Sequence 3, Appl
21	16.8	84.0	15660	US-10-138-588-19	Sequence 19, Appl
22	16.8	84.0	16557	US-11-049-637-1	Sequence 1, Appl
23	16.8	84.0	16908	US-10-451-168-27	Sequence 27, Appl

24	16.8	84.0	16908	9	US-10-980-387-27	Sequence 27, Appl
25	16.8	84.0	18207	9	US-10-934-998-30	Sequence 30, Appl
26	16.8	84.0	18209	9	US-10-773-446-56	Sequence 66, Appl
27	16.8	84.0	18248	8	US-10-723-860-5390	Sequence 5390, App
28	16.8	84.0	51806	8	US-10-719-993-6892	Sequence 6892, App
29	16.8	84.0	12393	6	US-10-311-455-1235	Sequence 1235, App
30	15.8	79.0	529	8	US-10-425-115-158964	Sequence 158964, A
31	15.8	79.0	728	7	US-10-437-963-69641	Sequence 89641, A
32	15.8	79.0	972	7	US-10-282-122A-32124	Sequence 32124, A
33	15.8	79.0	5352	10	US-11-097-143-18581	Sequence 18581, A
34	15.8	79.0	9545	10	US-11-097-143-18580	Sequence 18580, A
35	15.8	79.0	15303	7	US-10-668-767-145	Sequence 145, App
36	15.8	79.0	15387	7	US-10-668-767-127	Sequence 127, App
37	15.8	79.0	15405	7	US-10-668-767-129	Sequence 129, App
38	15.8	79.0	15429	7	US-10-668-767-143	Sequence 143, App
39	15.8	79.0	15679	7	US-10-668-767-1	Sequence 1, Appl
40	15.8	79.0	9025608	6	US-10-156-763-1	Sequence 1, Appl
41	15.4	77.0	7401	10	US-11-097-143-26002	Sequence 26002, A
42	15.2	76.0	424	7	US-10-424-599-135092	Sequence 135092, A
43	15.2	76.0	532	6	US-10-029-386-9824	Sequence 9824, App
44	15.2	76.0	585	8	US-10-425-115-47123	Sequence 47123, A
45	15.2	76.0	645	8	US-10-425-115-115036	Sequence 115036, A

ALIGNMENTS

RESULT 1
US-09-735-995-60
Sequence 60, Application US/09735995
Patent No. US20010034024A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
TITLE OF INVENTION: SYNDROME GENE
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/735,995
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/226,012
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 60
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-735-995-60

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCGTCACGCGCACTCT 20
Db 1 GGTCCGTCACGCGCACTCT 20

RESULT 2
US-10-696-708-60
Sequence 60, Application US/10696708
Publication No. US20040078833A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
FILE REFERENCE: 2323-164
CURRENT APPLICATION NUMBER: US/10/696,708
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 09/735,995
PRIOR FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: US 09/226,012

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; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 09/122,847
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-696-708-60

Query Match          100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTCCCGTCAGCGCACTCT 20
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Db       1  GGTCCCGTCAGCGCACTCT 20

RESULT 3
US-10-934-998-252
; Sequence 252, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-MAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
; FILE REFERENCE: BMA-04-1206
; CURRENT APPLICATION NUMBER: US/10/934,998
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: FR02/02717
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/04546
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 252
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer GY29-1
US-10-934-998-252

Query Match          84.0%; Score 16.8; DB 9; Length 29;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCCCGTCAGCGCACTCT 20
        |||||
Db       1  GGTCCCGTCAGCGCACTCT 29

RESULT 4
US-10-719-993-6589
; Sequence 6589, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6589
; LENGTH: 201
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6589

Query Match          84.0%; Score 16.8; DB 8; Length 201;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCCCGTCAGCGCACTCT 20
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Db       1  GGTCCCGTCAGCGCACTCT 200

RESULT 5
US-10-719-993-6593
; Sequence 6593, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6593
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6593

Query Match          84.0%; Score 16.8; DB 8; Length 201;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCCCGTCAGCGCACTCT 20
        |||||
Db       1  GGTCCCGTCAGCGCACTCT 99

RESULT 6
US-10-719-993-41420
; Sequence 41420, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41420
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-41420

Query Match          84.0%; Score 16.8; DB 8; Length 201;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCCCGTCAGCGCACTCT 20
        |||||
Db       1  GGTCCCGTCAGCGCACTCT 200

RESULT 7
US-10-719-993-41474
; Sequence 41474, Application US/10719993
; Publication No. US20040265849A1
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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2003-11-24
; CURRENT APPLICATION NUMBER: US/10/719,993
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 41474
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-41474

Query Match          84.0%; Score 16.8; DB 8; Length 201;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      80 GGTCCCTGTCAAGCGCACTCT 99

RESULT 8
US-10-934-998-131/c
; Sequence 131, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-MAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; FILE REFERENCE: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
; CURRENT FILING DATE: 2004-09-03
; CURRENT APPLICATION NUMBER: US/10/934,998
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/02717
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: FR02/04546
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 131
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-934-998-131

Query Match          84.0%; Score 16.8; DB 9; Length 564;
Best Local Similarity 90.0%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      564 GGTCCCGTCACGCGCACTCT 545

RESULT 9
US-10-425-115-87910
; Sequence 87910, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 87910
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: M8T4577_180173C.1
US-10-425-115-87910

Query Match          84.0%; Score 16.8; DB 8; Length 1851;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      1153 GGTCCCGTCACGCGCACTCT 1172

RESULT 10
US-10-138-588-17
; Sequence 17, Application US/10138588
; Publication No. US20040018594A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
; FILE REFERENCE: ENCODING THE ANTIGENS, AND METHODS OF USE
; CURRENT FILING DATE: 2002-05-01
; CURRENT APPLICATION NUMBER: US/10/138,588
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/288,395
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/308,901
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,388
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/324,757
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/288,900
; NUMBER OF SEQ ID NOS: 203
; SEQ ID NO: 17
; LENGTH: 2153
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(2137)
US-10-138-588-17

Query Match          84.0%; Score 16.8; DB 7; Length 2153;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      1265 GGTCCCGTCACGCGCACTCT 1284

RESULT 11
US-09-814-353-21856
; Sequence 21856, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT FILING DATE: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
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      ; PRIOR APPLICATION NUMBER: 09/540,217
      ; PRIOR FILING DATE: 2000-03-31
      ; PRIOR APPLICATION NUMBER: 09/649,167
      ; PRIOR FILING DATE: 2000-08-23
      ; NUMBER OF SEQ ID NOS: 60736
      ; SOFTWARE: Custom
      ; SEQ ID NO 3924
      ; LENGTH: 3910
      ; TYPE: DNA
      ; ORGANISM: Homo sapiens
      ; FEATURE:
      ; NAME/KEY: SIMILAR
      ; LOCATION: (3497)..(3649)
      ; OTHER INFORMATION: 29% homologous to Caenorhabditis elegans hemicentin
      ; OTHER INFORMATION: precursor accession number AF074901, Smith-Waterman Score=45
US-10-450-763-3924

Query Match          84.0%; Score 16.8; DB 9; Length 3910;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY       1 GGTCGGCTCACGCGCACTT 20
        |||||             |||||
Db        2573 GGTCGGCTCAAAGGCAC T 2592

RESULT 14
US-10-019-065A-34
; Sequence 34, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCR
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 4073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-019-065A-34

Query Match          84.0%; Score 16.8; DB 7; Length 4073;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY       1 GGTCGGCTCACGCGCACTT 20
        |||||             |||||
Db        1799 GGTCGGCTCAAAGGCAC T 1818

RESULT 15
US-10-115-479-87
; Sequence 87, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithsonian, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voess, Edward
```

APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shinkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 87
LENGTH: 5935
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(5860)
US-10-115-479-87

Query Match 84.0%; Score 16.8; DB 6; Length 5935;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCGTCACGCGCACTCT 20
|||||
Db 2663 GATCCGTCACGCGCACTCT 2682

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Job time : 448 secs

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 15:02:55 ; Search time 76 Seconds
(without alignments)
467.779 Million cell updates/sec

Title: US-10-696-708A-60
Perfect score: 20
Sequence: 1 ggtccgcgcacgcgacctc 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-226-012-60
2	16.8	84.0	12381	3	US-09-953-096-3
3	16.8	84.0	16557	3	US-09-953-096-1
4	15.8	79.0	652	3	US-09-270-767-10499
5	15.8	79.0	711	3	US-09-489-039A-4679
6	15.4	77.0	1196	3	US-09-270-767-5074
7	15.4	77.0	1196	3	US-09-270-767-20356
8	15.2	76.0	452	3	US-09-621-976-3072
9	15.2	76.0	601	3	US-09-949-016-142055
10	15.2	76.0	994	3	US-09-775-358-70
11	15.2	76.0	1237	2	US-08-240-372-1
12	15.2	76.0	1535	3	US-09-668-680-12
13	15.2	76.0	14462	3	US-09-902-540-1090
14	15.2	76.0	14462	3	US-09-902-540-9597
15	15.2	76.0	363032	3	US-09-949-016-12415
16	15.2	76.0	363033	3	US-09-949-016-15754
17	15	75.0	26492	3	US-09-902-540-1234
18	14.8	74.0	888	3	US-09-134-000C-1221
19	14.8	74.0	967	3	US-09-270-767-2133
20	14.8	74.0	967	3	US-09-270-767-17415
21	14.8	74.0	4107	3	US-09-902-540-2552
22	14.8	74.0	15377	3	US-09-902-540-1116
23	14.4	72.0	601	3	US-09-949-016-58791
24	14.4	72.0	601	3	US-09-949-016-58792

25	14.4	72.0	633	3	US-08-818-112-6	Sequence 6, Appli
26	14.4	72.0	633	3	US-08-818-111-6	Sequence 6, Appli
27	14.4	72.0	633	3	US-09-056-556-6	Sequence 6, Appli
28	14.4	72.0	633	3	US-09-072-596-6	Sequence 6, Appli
29	14.4	72.0	633	3	US-09-072-967-6	Sequence 6, Appli
30	14.4	72.0	633	3	US-10-193-002-6	Sequence 6, Appli
31	14.4	72.0	633	3	US-10-084-843-6	Sequence 6, Appli
32	14.4	72.0	804	3	US-09-902-540-5172	Sequence 5172, Ap
33	14.4	72.0	1488	3	US-09-711-164-267	Sequence 267, App
34	14.4	72.0	1488	3	US-09-902-540-8761	Sequence 8761, Ap
35	14.4	72.0	9333	3	US-09-902-540-930	Sequence 930, App
36	14.4	72.0	29559	3	US-09-902-540-1254	Sequence 1254, Ap
37	14.4	72.0	57103	3	US-09-949-016-13445	Sequence 13445, A
38	14.2	71.0	145	3	US-09-513-999C-16720	Sequence 16720, A
39	14.2	71.0	375	3	US-09-621-976-2120	Sequence 2120, Ap
40	14.2	71.0	491	3	US-09-270-767-8856	Sequence 8856, Ap
41	14.2	71.0	491	3	US-09-270-767-24138	Sequence 24138, A
42	14.2	71.0	500	3	US-09-827-998-64	Sequence 64, Appli
43	14.2	71.0	601	3	US-09-949-016-29417	Sequence 29417, A
44	14.2	71.0	601	3	US-09-949-016-29418	Sequence 29418, A
45	14.2	71.0	601	3	US-09-949-016-40713	Sequence 40713, A

ALIGNMENTS

```
RESULT 1
US-09-226-012-60
Sequence 60, Application US/09226012
Patent No. 6207383
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226.012
CURRENT FILING DATE: 1999-01-06
EARLIER APPLICATION NUMBER: 09/122.847
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 60
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-226-012-60

Query Match      100.0%; Score 20; DB 3; Length 20;
Beet Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
DB      1 GGTCCCGTCACGCGCACTCT 20

RESULT 2
US-09-953-096-3
Sequence 3, Application US/09953096
Patent No. 6867291
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Donoho, Gregory
TITLE OF INVENTION: No. 6867291e1 Human Hemiscentin Proteins and Polynucleotides Encod
FILE REFERENCE: LEX-0235-USA
CURRENT APPLICATION NUMBER: US/09/953.096
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/232.793
PRIOR FILING DATE: 2000 09-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 3
; LENGTH: 12381
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-953-096-3

Query Match 84.0%; Score 16.8; DB 3; Length 12381;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCAGCGGCACTCT 20
|||||
Db 9242 GGTCCCGTCAGCGGCACTCT 9261

RESULT 3
US-09-953-096-1
; Sequence 1, Application US/09953096
; Patent No. 6867291
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. 6867291el Human Hemiscentin Proteins and Polynucleotides Encod
; FILE REFERENCE: Lex-0235-USA
; CURRENT APPLICATION NUMBER: US/09/953, 096
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/232,793
; PRIOR FILING DATE: 2000 09-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16557
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-953-096-1

Query Match 84.0%; Score 16.8; DB 3; Length 16557;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCAGCGGCACTCT 20
|||||
Db 13418 GGTCCCGTCAGCGGCACTCT 13437

RESULT 4
US-09-270-767-10499/C
; Sequence 10499, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10499
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10499

Query Match 79.0%; Score 15.8; DB 3; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCCGTCAGCGGCACTCT 20
|||||
Db 294 GTCCCGTCAGCGGCACTTT 276

RESULT 5
US-09-489-039A-4679
; Sequence 4679, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4679
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4679

Query Match 79.0%; Score 15.8; DB 3; Length 711;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCAGCGGCACTC 19
|||||
Db 484 GGTCCCGTCAGCGGCACTC 502

RESULT 6
US-09-270-767-5074/C
; Sequence 5074, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5074
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5074

Query Match 77.0%; Score 15.4; DB 3; Length 1196;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCGGTACGCGGCACTCT 20
|||||
Db 1182 CCGGTACGCGGCACTCT 1166

RESULT 7
US-09-270-767-20356/C
; Sequence 20356, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20356
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20356

Query Match 77.0%; Score 15.4; DB 3; Length 1196;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCGTCACGGCCGACTCT 20
DB 1182 CCGGTACGCGCCTCT 1166

RESULT 8
US-09-621-976-3072/c
; Sequence 3072, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3072
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..240
US-09-621-976-3072

Query Match 76.0%; Score 15.2; DB 3; Length 452;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCGGTCACGGCCTCT 20
DB 381 GGGCCCGTCACGGCCTCT 362

RESULT 9
US-09-949-016-142055
; Sequence 142055, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142055
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142055

Query Match 76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCGGTCACGGCCTCT 20
||||| ||||| |||||

DB 38 GGTCGGTCACGGCCTCTT 57

RESULT 10
US-09-775-398-70/c
; Sequence 70, Application US/09775398
; Patent No. 6893820
; GENERAL INFORMATION:
; APPLICANT: Pias, Christoph
; TITLE OF INVENTION: Detection of Methylated CpG Rich Sequences Diagnostic for Maligna
; FILE REFERENCE: 22727/04075
; CURRENT APPLICATION NUMBER: US/09/775,398
; CURRENT FILING DATE: 2001-01-04
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 70
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Homo sapiens 4.D.12
; FEATURE:
; NAME/KEY: n
; LOCATION: (673)..(673)
; OTHER INFORMATION: a or g or c or t
; NAME/KEY: n
; LOCATION: (686)..(686)
; OTHER INFORMATION: a or g or c or t
; NAME/KEY: n
; LOCATION: (701)..(701)
; OTHER INFORMATION: a or g or c or t
; NAME/KEY: n
; LOCATION: (754)..(754)
; OTHER INFORMATION: a or g or c or t
; NAME/KEY: n
; LOCATION: (764)..(764)
; OTHER INFORMATION: a or g or c or t
; NAME/KEY: n
; LOCATION: (774)..(774)
; OTHER INFORMATION: a or g or c or t
US-09-775-398-70

Query Match 76.0%; Score 15.2; DB 3; Length 994;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCGGTCACGGCCTCT 20
DB 252 GGTCGGTCACGGCCTCT 233

RESULT 11
US-08-240-372-1/c
; Sequence 1, Application US/08240372
; Patent No. 5741665
; GENERAL INFORMATION:
; APPLICANT: KATO, ELIE K.
; APPLICANT: STUART, W. DORSEY
; TITLE OF INVENTION: LIGHT-REGULATED PROMOTERS FOR PRODUCTION
; NUMBER OF INVENTION: OF HETEROLOGOUS PROTEINS IN FILAMENTOUS FUNGI
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,372
; FILING DATE: 10-MAY-1994

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 3918-0003.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1237 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-240-372-1

Query Match          76.0%; Score 15.2; DB 2; Length 1237;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      506 GATCCCGTCTCGCGCCTCT 487

RESULT 12
US-09-668-680-12
; Sequence 12, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xu, Aiding J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790C1P2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_Fl_genes Version 2.0
; SEQ ID NO 12
; LENGTH: 1535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1338)
;
US-09-668-680-12

Query Match          76.0%; Score 15.2; DB 3; Length 1535;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      720 GGTCCCGTCACGCGCCTCT 739

RESULT 13
US-09-902-540-1090
; Sequence 1090, Application US/09902540
; Patent No. 6833447
```

```

; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1090
; LENGTH: 14462
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
;
US-09-902-540-1090

Query Match          76.0%; Score 15.2; DB 3; Length 14462;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      12680 GGTCCCGTCTACGCGCCTCT 12699

RESULT 14
US-09-902-540-9597
; Sequence 9597, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9597
; LENGTH: 14462
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
;
US-09-902-540-9597

Query Match          76.0%; Score 15.2; DB 3; Length 14462;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGTCCCGTCACGCGCACTCT 20
Db      12680 GGTCCCGTCTACGCGCCTCT 12699

RESULT 15
US-09-949-016-12415/C
; Sequence 12415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
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; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 12415
 ; LENGTH: 363032
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)_(363032)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-12415

Query Match 76.0%; Score 15.2; DB 3; Length 363032;
 Best Local Similarity 85.0%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGTCCTGTCACGCGCACTCT 20
 |||||
 Db 355418 GGTCCTGTCACGCGCACTTT 355399

Search completed: April 10, 2006, 15:05:36
 Job time : 78 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 14:57:22 ; Search time 1563.5 Seconds
(without alignments)
598.492 Million cell updates/sec

Title: US-10-696-708a-60
Perfect score: 20
Sequence: 1 ggtccgcgcacgcacacct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.8	84.0	211	8 H21884	H21884 y134e11.r1
2	16.8	84.0	226	10 C2917270	C2917270 4021005A0
3	16.8	84.0	387	10 CG464694	CG464694 KRIBB_2D_
4	16.8	84.0	493	2 BE207204	BE207204 dal3e01.y
5	16.8	84.0	507	2 BF059067	BF059067 7K37402.x
6	16.8	84.0	534	9 AQ338091	AQ338091 HS_5011.B
7	16.8	84.0	547	7 CK685362	CK685362 ZF101-P00
8	16.8	84.0	596	7 CK679806	CK679806 ZF101-P00
9	16.8	84.0	624	8 DR448434	DR448434 AR1055F05
10	16.8	84.0	659	8 DR442497	DR442497 AR2005D08
11	16.8	84.0	694	7 CN200871	CN200871 Tor10541
12	16.8	84.0	733	7 CN208435	CN208435 Tor8923.G
13	16.8	84.0	737	10 CG003293	CG003293 ZUABY27TV
14	16.8	84.0	793	7 CN206743	CN206743 Tor7169.G
15	16.8	84.0	794	7 CN202185	CN202185 Tor2313.G
16	16.8	84.0	800	10 CG390264	CG390264 ZMMBB057
17	16.8	84.0	816	5 BU747235	BU747235 CH34010.C
18	16.8	84.0	820	7 CN204936	CN204936 Tor5324.G
19	16.8	84.0	833	7 CO926788	CO926788 AGENCOURT
20	16.8	84.0	834	7 CN208937	CN208937 Tor9445.G
21	16.8	84.0	836	10 C2300703	C2300703 ZMMBF0074
22	16.8	84.0	875	9 CC649591	CC649591 OGMCH17TV

23	16.8	84.0	907	10 C2334451	C2334451 ZMMBF0043
24	16.8	84.0	956	10 CL285801	CL285801 ZMMBB063
25	16.8	84.0	4962	4 HSM804543	AL833232 Homo sapi
26	16.8	84.0	8022	11 D0037948	D0037948 Homo sapi
27	16.8	84.0	8022	11 D0037949	D0037949 Pan trogl
28	16.8	84.0	216	2 BF670386	BF670386 602150265
29	16.8	84.0	675	3 BI955119	BI955119 HVSMB002
30	16.4	82.0	875	9 CC643962	CC643962 OGOAC36TC
31	16.4	82.0	910	9 CC643968	CC643968 OGOAC36TM
32	16.4	82.0	935	11 CNS04G03	AL289884 Tetradodon
33	16.4	82.0	1087	10 CM925592	CM925592 EDCBBS3TF
34	16	80.0	221	11 TH134F11Q	AL466443 T. brucei
35	16	80.0	261	8 W15079	W15079 T1726 MWAT4
36	16	80.0	337	9 B54696	B54696 CIT-HSP-384
37	16	80.0	410	2 BG075801	BG075801 H3152A03-
38	16	80.0	487	16 AJ234088	AJ234088 B927 036
39	16	80.0	526	11 TH317D09Q	AT491463 T. brucei
40	16	80.0	528	11 TH356A01P	AT497090 T. brucei
41	16	80.0	549	9 AQ941653	AQ941653 Sheared D
42	16	80.0	571	10 CG186409	CG186409 PUIGL56TD
43	16	80.0	645	9 A0658336	A0658336 Sheared D
44	16	80.0	707	3 BM684541	BM684541 UI-E-EJO-
45	16	80.0	710	5 BU283768	BU283768 603664203

ALIGNMENTS

RESULT 1
H21884
LOCUS
DEFINITION
y134e11.r1 Soares breast 3mHbSt Homo sapiens cDNA clone
IMAGE:160172.5, similar to SP:NCA3 MOUSE P13594 NEURAL CELL
ADHESION PROTEIN, SECRETED ISOFORM PRECURSOR ; mRNA sequence.

ACCESSION
H21884
VERSION
H21884.1 GI:890579
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Hillier, L., Clark, N., Dubuque, T., Ellisston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Metra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterson, R., Williamson, A., Woldmann, P. and
Wilson, R.

TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Insert Size: 951
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGS Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert Length: 951 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.

FEATURES
source
1..211
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:578597"
/db_xref="taxon:9606"

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/clone="IMAGE:160172"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3bHbact"
/notes="Organ: breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCACTGAGTGGAGCGCGCCGCTTTTCTTTTCTT 3').
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match      84.0%; Score 16.8; DB 8; Length 211;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1  GGTCCCGTCACGCGCACTCT 20
        |||||
Db      186 GGTCCCGTCACGCGCACTCT 205

RESULT 2
LOCUS   C2917270      226 bp    DNA      linear    GSS 08-AUG-2005
DEFINITION 4021005A02.x1 4021 - RescuenMu Grid V Zea mays genomic, genomic
survey sequence.
ACCESSION C2917270
VERSION   C2917270.1 GI:71935939
KEYWORDS GSS.
SOURCE    Zea mays
ORGANISM  Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoidae; Andropogoneae; Zea.
          1 (bases 1 to 226)
          Walbot, V.
REFERENCE Maize genomic sequences found using engineered RescuenMu transposon
AUTHORS   Unpublished (2001)
TITLE     Contact: Walbot V
JOURNAL   Department of Biological Sciences
COMMENT   Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 4021005 column: 45
          Class: transposon-tagged.
FEATURES
  source
    1..226
      /organism="Zea mays"
      /mol_type="genomic DNA"
      /culturvar="mixed background W23/A188/B73/K55"
      /db_xref="taxon:4577"
      /tissue_type="leaf"
      /dev_stage="adult"
      /lab_host="DH10B"
      /clone_lib="4021 - RescuenMu Grid V"
      /note="Organ: leaf; Vector: RescuenMu (engineered from
      pBluescript backbone); Site_1: BamHI; Site_2: BglII;
      RescuenMu is a 4.9 kb, modified maize Mu transposon
      designed to allow plasmid rescue from total genomic DNA.
      Mu elements insert preferentially into transcription
      units. For more information on RescuenMu, go to the web
      site 'http://www.mutransposon.org/project/RescuenMu/'. Grid
      V was grown at University of Arizona in 2003. DNA was
      extracted from leaf strips, double digested using BamHI
      and BglII, and ligated to form circular plasmids. DH10B
      cells were transformed and then screened on LB plates with

```

```

ORIGIN      ampicillin."

Query Match      84.0%; Score 16.8; DB 10; Length 226;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1  GGTCCCGTCACGCGCACTCT 20
        |||||
Db      195 GGTCCCGTCACGCGCACTCT 214

RESULT 3
LOCUS   CG464694/c      387 bp    DNA      linear    GSS 24-SEP-2003
DEFINITION KRIIB 2D B25T7 PBS-NE Library Homo sapiens genomic clone
KRIIB_2D_B25_5, genomic survey sequence.
ACCESSION CG464694
VERSION   CG464694.1 GI:35188129
KEYWORDS GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
          1 (bases 1 to 387)
          Lee,K.T., Kim,J.H., Hahn,Y.S., Yang,J.O., Chu,M.Y., Kim,H.C.,
          Oh,K.J., Kim,S.S., Yoo,H.S. and Kim,Y.S.
          Rapid isolation of NotI-linked CpG island sequences from RUGS gel
          Unpublished (2003)
REFERENCE Human Genome Research Laboratory
AUTHORS   Human Genome Research Laboratory
          52 Eoeun-dong, Yuseong-gu, Daejeon 305-333, Republic of Korea
          Tel: 82-42-879-8110
          Fax: 82-42-879-8119
          Email: yongsung@kribb.re.kr
          This result was produced by the program for Functional Analysis of
          Human Genome funded from Ministry of Science and Technology,
          Republic of Korea. Clones are available from the Center for
          Functional Analysis of Human Genome. See URL:
          http://21cgenome.kribb.re.kr/ for details or contact:
          yongsung@kribb.re.kr
          Seq primer: T7 primer
          Class: NotI site
          High quality sequence stop: 387.
FEATURES
  source
    1..387
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /clone="KRIIB_2D_B25"
      /sex="male"
      /tissue_type="blood"
      /dev_stage="adult"
      /clone_lib="PBS-NE library"
      /note="Vector: pBluescriptKS(+); Site_1: NotI; Site_2:
      EcoRV; Genomic DNA was digested with NotI and EcoRV and
      the resulting fragments were ligated into ZAPIT/NotI
      vector DNA. After the digestion with EcoRV, the mixture
      was run on 0.8% LMP agarose gel, eluted a gel portion over
      22 kb and purified with beta-agarase I. The purified DNA
      was digested with NotI, run on 1% LMP agarose gel, and
      eluted with Gel Extraction kit the DNA fragments ranging
      0.7 to 4 kb, which cover on first-dimensional gel
      comprising the central portion of the standard RUGS
      profile. The DNA solution was ligated into pBluescript
      KS(+) with NotI and EcoRV ends. The ligated solution was
      transformed into DH5a cell using electroporation machine."
ORIGIN

Query Match      84.0%; Score 16.8; DB 10; Length 387;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;

```


Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTCCCGTCACGCGCACTCT 20
|||||
Db 214 GGTCTGTGACGCGCACTCT 195

RESULT 4
BE207204/c
LOCUS
DEFINITION
493 bp mRNA linear EST 27-JUN-2000
ba13601.Y1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:2824248 5'
similar to WP:FO8B2.9 CE13435 PHENYLALANYL-TRNA SYNTHETASE ;, mRNA
sequence.

ACCESSION
BE207204
VERSION
BE207204.1 GI:8750602
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library
Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
image.llnl.gov/image/htcml/resources.shtm1

FEATURES
source
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..493
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2824248"
/cissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 493;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTCCCGTCACGCGCACTCT 20
|||||
Db 328 GGGCCCGTCACGCGCACTCT 309

RESULT 5
BF059067/c
LOCUS
DEFINITION
507 bp mRNA linear EST 16-OCT-2000
7k37d02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3477554 3',
mRNA sequence.

ACCESSION
BF059067
VERSION
BF059067.1 GI:10812963

KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
1..507
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3477554"
/cissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGCGACATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 507;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTCCCGTCACGCGCACTCT 20
|||||
Db 198 GGTCTGTGACGCGCACTCT 179

RESULT 6
AQ338091
LOCUS
DEFINITION
534 bp DNA linear GSS 06-MAR-1999
HS 5011 B1 A04 T7 RPII1 Human Male BAC Library Homo sapiens
genomic clone Plate=587 Col=7 Row=B, genomic survey sequence.

ACCESSION
AQ338091
VERSION
AQ338091.2 GI:4341992
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 534)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764

COMMENT On Feb 19, 1999 this sequence version replaced gi:4144107.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htesc.washington.edu
Plate: 587 row: B column: 7
Seq primer: T7
Class: BAC ends
High quality sequence stop: 534.
Location/Qualifiers
1..534
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=587 Col=7 Row=B"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC11 Human Male BAC Library"
/note="Vector: pBACe3.6; RPC11 Human Male BAC Library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 534;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCCCGTCACGCGCACTCT 20
|||||
Db 371 GGTCCGTGTACGCGCACTCT 390

RESULT 7
CK685362/c 547 bp mRNA linear EST 30-MAR-2004
LOCUS ZF101-P00037-DEPE-F2_D17 GISZF001_ra Dantio rerio cDNA clone
DEFINITION IMAGE:7147939 5', mRNA sequence.
CK685362
ACCESSION CK685362.1 GI:42437698
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Dantio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 547)
Weil,C., Mathavan,S., Thoreau,H., Lim,L., Lee,C. and Ruan,Y.
Genome Institute of Singapore, Zebrafish Gene Collection
Unpublished (2004)
Contact: Ruan Y
Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tel: +65 6478 8073
Fax: +65 6478 9059
Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00037-BR2_D17
PCR Primers
FORWARD: M13
BACKWARD: M13
Plate: ZF101-P00037-BR2 row: D column: 17
Seq primer: CCGCATTAAGTGTATAGCA
High quality sequence stop: 547.
Location/Qualifiers
1..547
/organism="Danio rerio"
/mol_type="mRNA"
/strain="Singapore local strain"
/db_xref="taxon:7955"
/clone="IMAGE:7147939"

FEATURES
source

/tissue_type="Embryo"
/dev_stage="7 Different embryonic Stages (From just
fertilized Embryos to 72 hours just hatched baby fish)"
/lab_host="DH10B"
/clone_lib="GISZF001_ra"
/note="Vector: pDNR-LIB; site 1: Sfi A (GGCCATTAGCGCC);
site 2: Sfi B (GGCCAGCGCGCC); Priming method: Sfi-(dt)30
primed; Priming sequence:
5.ATTCTAGAGCGCGAGCGCCGACATG(T)30VN; directionally
cloned, 5' cloning site: Sfi A site GGCCATTAGCGCC; 5'
linker/adaptor sequence: 5.AAGCAGGTGATCAACCGAGTGGCC;
3' cloning site: Sfi B site GGCCAGCGCGCC; 3'
linker/adaptor sequence: same as the priming sequence;
Average insert size: 2kb; For PCR insert analysis: Use
M13 Forward and reverse primers; Library Amplified;
Recombinants (inserts): 98%; Library complexity: 5x10⁶;
Full-length construction (method): SMART, a Clontech
method The pooled tissue RNA was collected and used to
construct full length enriched cDNA library and also
served as template to synthesize cDNA first strand cDNA
probe. Two high density colony arrays were made from over
110K cDNA clones and hybridized with the probes. Low
intensity clones were selected as they represented rare
expressed clones. The hybridization intensities for all
clones span from 0 to 1.8 million counts and the low
abundant class ranged from 0 to 13,000."

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 547;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCCCGTCACGCGCACTCT 20
|||||
Db 307 GGTCCAGTTCACGCGCACTCT 288

RESULT 8
CK679806/c 596 bp mRNA linear EST 30-MAR-2004
LOCUS ZF101-P00018-DEPE-F N04 GISZF001_ra Dantio rerio cDNA clone
DEFINITION IMAGE:7141254 5', mRNA sequence.
CK679806
ACCESSION CK679806.1 GI:42431958
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Dantio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 596)
Weil,C., Mathavan,S., Thoreau,H., Lim,L., Lee,C. and Ruan,Y.
Genome Institute of Singapore, Zebrafish Gene Collection
Unpublished (2004)
Contact: Ruan Y
Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tel: +65 6478 8073
Fax: +65 6478 9059
Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00018-BR2_N04
PCR Primers
FORWARD: M13
BACKWARD: M13
Plate: ZF101-P00018-BR2 row: N column: 04
Seq primer: CCGCATTAAGTGTATAGCA
High quality sequence stop: 596.
Location/Qualifiers
1..596
/organism="Danio rerio"
/mol_type="mRNA"
/strain="Singapore local strain"

FEATURES
source

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/db_xref="taxon:7955"
/clone="IMAGE:7141254"
/tissue_type="Embryo"
/dev_stage="7 Different embryonic Stages(from just fertilized Embryos to 72 hours just hatched baby fish)"
/lab_host="VDH10B"
/clone_lib="GISZFP001.ra"
/notes="vector: pDNR-LIB; Site_1: Sfi A (GGCCATTACGGCC); Site_2: Sfi B (GGCCGAGCGGCC); Priming method: Sfi-(dT)30 primed; Priming sequence: 5.ATTCTAGACCGGCGCGCCAGT(7)30VN; Directionally cloned, 5' cloning site: Sfi A site GGCCATTACGGCC; 5' linker/adaptor sequence: 5.AGCAGTGTATCAACGAGTGTGACC; 3' cloning site: Sfi B site GGCCGAGCGGCC; 3' linker/adaptor sequence: same as the priming sequence; Average insert size: 2kb; For PCR insert analysis: Use M13 Forward and reverse primers; Library complexity: 5x106; Recombinants (inserts): 98%; Library complexity: 5x106; Full-length construction (method): SMART, a Clontech method The pooled tissue RNA was collected and used to construct full length enriched cDNA library and also served as template to synthesize complex first strand cDNA probe. Two high density colony arrays were made from over 110K cDNA clones and hybridized with the probes. Low intensity clones were selected as they represented rare expressed clones. The hybridization intensities for all clones span from 0 to 1.8 million counts and the low abundant class ranged from 0 to 13,000."

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ORIGIN

```

Query Match      84.0%; Score 16.8; DB 7; Length 596;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

Qy      1  GGTCCCGTCACGCGCACTCT 20
        |||||
Db      283 GGTCCAGTCACGCGCACTCT 264

```

```

RESULT 9
DR448434/c      624 bp      mRNA      linear      EST 05-JUL-2005
LOCUS      DR448434
DEFINITION      AR1055F05 A. gomesiana hemocytes normalized library Acanthoscurria gomesiana cDNA clone AR1055F05 5', mRNA sequence.
ACCESSION      DR448434
VERSION        DR448434.1
KEYWORDS       GI:68770098
SOURCE         EST.
ORGANISM       Acanthoscurria gomesiana
               Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
               Mygalomorphae; Theraphosidae; Acanthoscurria.
REFERENCE      1 (bases 1 to 624)
AUTHORS        Lorenzini,D.M., Silva,P.I. Jr., Soares,M.B., Arruda,P., Setubal,J.
               and Daffre,S.
TITLE          Discovery of immune related genes expressed on hemocytes of the tarantula spider Acanthoscurria gomesiana
JOURNAL        Unpublished (2005)
COMMENT        Contact: Daffre S
               Departament of Parasitology, ICB
               University of Sao Paulo
               Av. Prof. Lineu Prestes, 1374, CEP 05508-900, Sao Paulo, SP, Brazil
               Tel: 55 11 3091 7272
               Fax: 55 11 3091 7417
               Email: sidadfref@icb.usp.br
               Seq primer: AATTACCTCCTACTAAAGG (T3)
               High quality sequence stop: 624.
               Location/Qualifiers
               1..624
               /organism="Acanthoscurria gomesiana"
               /mol_type="mRNA"
               /db_xref="taxon:115339"
               /clone="AR1055F05"
               /tissue_type="hemocytes"

```

FEATURES

source

```

/cell_type="hemocytes"
/dev_stage="adult"
/clone_lib="A. gomesiana hemocytes normalized library"
/notes="vector: pRTT3-Pac; Site_1: EcoRI; Site_2: NotI; normalized cDNA library. first strand synthesis with NotI-dT(18) primer. cDNAs > 350 bp selected by chromatography (Bio-Gel A50). double-stranded cDNAs ligated to EcoRI blunt adapter, digested with NotI, size selected (> 350 bp) and cloned into pRTT3-Pac vector. single-stranded plasmids hybridized with cDNA inserts at low Cot (approx 5), remaining single-stranded plasmids (normalized library) selected using a hydroxyapatite (HAP) column."

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ORIGIN

```

Query Match      84.0%; Score 16.8; DB 8; Length 624;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1  GGTCCCGTCACGCGCACTCT 20
        |||||
Db      268 GGTCCAGTCACGCGCACTGT 249

```

```

RESULT 10
DR442497      659 bp      mRNA      linear      EST 05-JUL-2005
LOCUS      DR442497/c
DEFINITION      AR2005D08 A. gomesiana hemocytes library Acanthoscurria gomesiana cDNA clone AR2005D08 5', mRNA sequence.
ACCESSION      DR442497
VERSION        DR442497.1
KEYWORDS       GI:68758988
SOURCE         EST.
ORGANISM       Acanthoscurria gomesiana
               Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
               Mygalomorphae; Theraphosidae; Acanthoscurria.
REFERENCE      1 (bases 1 to 659)
AUTHORS        Lorenzini,D.M., Silva,P.I. Jr., Soares,M.B., Arruda,P., Setubal,J.
               and Daffre,S.
TITLE          Discovery of immune related genes expressed on hemocytes of the tarantula spider Acanthoscurria gomesiana
JOURNAL        Unpublished (2005)
COMMENT        Contact: Daffre S
               Departament of Parasitology, ICB
               University of Sao Paulo
               Av. Prof. Lineu Prestes, 1374, CEP 05508-900, Sao Paulo, SP, Brazil
               Tel: 55 11 3091 7272
               Fax: 55 11 3091 7417
               Email: sidadfref@icb.usp.br
               Seq primer: AATTACCTCCTACTAAAGG (T3)
               High quality sequence stop: 659.
               Location/Qualifiers
               1..659
               /organism="Acanthoscurria gomesiana"
               /mol_type="mRNA"
               /db_xref="taxon:115339"
               /clone="AR2005D08"
               /tissue_type="hemocytes"
               /cell_type="hemocytes"
               /dev_stage="adult"
               /clone_lib="A. gomesiana hemocytes library"
               /notes="vector: pRTT3-Pac; Site_1: EcoRI; Site_2: NotI; -Pac vector."

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ORIGIN

```

Query Match      84.0%; Score 16.8; DB 8; Length 659;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

Qy      1  GGTCCCGTCACGCGCACTCT 20
        |||||
Db      164 GGTCCAGTCACGCGCACTGT 145

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RESULT 11
CN200871 694 bp mRNA linear EST 30-APR-2004
LOCUS Tort10541 Gametophyte rehydration library Tortula ruralis cDNA, mRNA
DEFINITION sequence.
ACCESSION CN200871.1 GI:46897602
VERSION CN200871.1
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Tortula ruralis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 694)
AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Maugeot,S.A. and Payton,P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbfk.ars.usda.gov
PCR primers
FORWARD: GTTTCCTCAGTCACGAC
BACKWARD: CAGGAACAGCTATGAC.
Location/Qualifiers
1..694
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
Salt; Site_2: NoTI"

ORIGIN
Query Match 84.0%; Score 16.8; DB 7; Length 694;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCACGCGCACTCT 20
|||||
317 GGTCCCGTCGCGGCACTCT 336

RESULT 12
CN208425 733 bp mRNA linear EST 30-APR-2004
LOCUS Tor8923 Gametophyte rehydration library Tortula ruralis cDNA, mRNA
DEFINITION sequence.
ACCESSION CN208425.1 GI:46905156
VERSION CN208425.1
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Tortula ruralis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 733)
AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Maugeot,S.A. and Payton,P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbfk.ars.usda.gov

PCR primers
FORWARD: GTTTCCTCAGTCACGAC
BACKWARD: CAGGAACAGCTATGAC.
Location/Qualifiers
1..733
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
Salt; Site_2: NoTI"

ORIGIN
Query Match 84.0%; Score 16.8; DB 7; Length 733;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCACGCGCACTCT 20
|||||
50 GGTCCCGTCGCGGCACTCT 69

RESULT 13
CG003293 737 bp DNA linear GSS 19-AUG-2003
LOCUS ZUA8Y27TV ZM.3_0.4_0_KB Zea mays genomic clone ZMMBPa0046F05,
DEFINITION genomic survey sequence.
ACCESSION CG003293
VERSION CG003293.1 GI:33873194
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 737)
AUTHORS Whitefaw,C.A., Quackenbush,J., Van Aken,S., Urtetack,T.,
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunez,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomice
JOURNAL Unpublished (2002)
COMMENT Other GSSs: ZUA8Y27RH
Contact: Cathy Whitefaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitefaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..737
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBPa0046F05"
/clone_lib="ZM.3_0.4_0_KB"
/note="Vector: pBOSK-; Site_1: HincII; 3-4 Kb 'unfiltered'
genomic DNA library"

ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 737;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCACGCGCACTCT 20
|||||
50 GGTCCCGTCGCGGCACTCT 69

RESULT 14
CN206743

LOCUS CN206743 793 bp mRNA linear EST 30-APR-2004
 DEFINITION Tor7169 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
 ACCESSION CN206743
 VERSION CN206743.1 GI:46903474
 KEYWORDS EST.
 SOURCE Tortula ruralis
 ORGANISM Tortula ruralis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Pottiaceae; Pottiaceae; Tortula.

REFERENCE
 AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
 TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
 Tortula ruralis: transcript classification and analysis
 JOURNAL BMC Genomics 5 (1), 89 (2004)
 PUBMED 15546486
 COMMENT Contact: Oliver Melvin J
 Plant Stress Lab
 USDA-ARS
 3810 4th St, Lubbock, TX 79415, USA
 Tel: 806-749-5560
 Fax: 806-723-5272
 Email: moliver@lbrk.ars.usda.gov
 PCR Primers
 FORWARD: GTTTCACGTCACGAC
 BACKWARD: CAGGAACAGCTATGAC.
 Location/Qualifiers
 1..793
 /organism="Tortula ruralis"
 /mol_type="mRNA"
 /db_xref="taxon:38588"
 /clone_lib="Gametophyte rehydration Library"
 /note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
 Salt; Site_2: NotI"

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 793;
 Best Local Similarity 90.0%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCACGCGCACTCT 20
 |||||
 DB 479 GGTCCCGTCGCGGCACTCT 498

RESULT 15
 CN202185 794 bp mRNA linear EST 30-APR-2004
 LOCUS CN202185
 DEFINITION Tor2313 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
 ACCESSION CN202185
 VERSION CN202185.1 GI:46898916
 KEYWORDS EST.
 SOURCE Tortula ruralis
 ORGANISM Tortula ruralis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Pottiaceae; Pottiaceae; Tortula.

REFERENCE
 AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
 TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
 Tortula ruralis: transcript classification and analysis
 JOURNAL BMC Genomics 5 (1), 89 (2004)
 PUBMED 15546486
 COMMENT Contact: Oliver Melvin J
 Plant Stress Lab
 USDA-ARS
 3810 4th St, Lubbock, TX 79415, USA
 Tel: 806-749-5560
 Fax: 806-723-5272
 Email: moliver@lbrk.ars.usda.gov
 PCR Primers
 FORWARD: GTTTCACGTCACGAC
 BACKWARD: CAGGAACAGCTATGAC.

FEATURES Location/Qualifiers
 source 1..794
 /organism="Tortula ruralis"
 /mol_type="mRNA"
 /db_xref="taxon:38588"
 /clone_lib="Gametophyte rehydration Library"
 /note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
 Salt; Site_2: NotI"

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 794;
 Best Local Similarity 90.0%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCCGTCACGCGCACTCT 20
 |||||
 DB 619 GGTCCCGTCGCGGCACTCT 638

Search completed: April 10, 2006, 16:03:27
 Job time : 1567.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 14:51:10 ; Search time 219.5 Seconds
(without alignments)
607.261 Million cell updates/sec

Title: US-10-696-708A-60

Perfect score: 1 ggtccgtcacgcgcactct 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*
- 14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	AAA07658
2	16.8	84.0	29	12	ADK60376
3	16.8	84.0	29	12	ADK60677
4	16.8	84.0	29	12	ADP73300
5	16.8	84.0	29	12	ADP73300
6	16.8	84.0	564	12	ADK60255
7	16.8	84.0	564	12	ADK60556
8	16.8	84.0	2136	12	ADH72103
9	16.8	84.0	2153	8	ACA10119
10	16.8	84.0	2153	12	ADH72101
11	16.8	84.0	2153	12	ADO08270
12	16.8	84.0	2517	10	ADC30192
13	16.8	84.0	3407	5	ADL63644
14	16.8	84.0	3910	5	AA568120
15	16.8	84.0	4073	6	AA172024
16	16.8	84.0	5877	12	ADL93996
17	16.8	84.0	5935	10	ADL93996
18	16.8	84.0	6024	12	ADK60301
19	16.8	84.0	6024	12	ADK60602

C	20	16.8	84.0	6024	12	ADP73225	Adp73225 Angiogene
	21	16.8	84.0	6343	8	ABX56304	Abx56304 Human NOV
	22	16.8	84.0	6343	12	ADH72107	Adh72107 Human gen
	23	16.8	84.0	8243	8	ABX56303	Abx56303 Human NOV
	24	16.8	84.0	8546	12	ADK60477	Adk60477 Angiogene
	25	16.8	84.0	8546	12	ADK60778	Adk60778 Angiogene
	26	16.8	84.0	8546	12	ADP73100	Adp73100 Angiogene
	27	16.8	84.0	8546	13	ADS09799	Ads09799 Human the
	28	16.8	84.0	8546	13	ADS98520	Ads98520 Protein f
	29	16.8	84.0	12381	14	ADY74313	Ady74313 Human hem
	30	16.8	84.0	12381	14	AE834667	Ae834667 Human hem
	31	16.8	84.0	15659	12	ADO08272	Ado08272 Human NOV
	32	16.8	84.0	15660	8	ACA10120	Act10120 Human NOV
	33	16.8	84.0	15660	12	ADH72105	Adh72105 Human gen
	34	16.8	84.0	16557	14	ADY74311	Ady74311 Human hem
	35	16.8	84.0	16557	14	AE834665	Ae834665 Human hem
	36	16.8	84.0	16908	6	ABO86156	Abog86156 Novel hum
	37	16.8	84.0	18207	12	ADK60455	Adk60455 Angiogene
	38	16.8	84.0	18207	12	ADK60756	Adk60756 Angiogene
	39	16.8	84.0	18207	12	ADP73078	Adp73078 Angiogene
	40	16.8	84.0	18209	14	AE894344	Aeb94344 Human hem
	41	16.8	84.0	18248	12	ADO22570	Ado22570 Human sof
	42	16.8	84.0	214019	10	ADL13809	Adl13809 Osteoearth
	43	16	80.0	12393	6	ABL33262	Ab133262 Human imm
	44	16	80.0	110000	14	AD242274_0	Ad242274 Human min
	45	15.8	79.0	711	11	ACH98884	Ach98884 Klebsiell

ALIGNMENTS

RESULT 1
ID AAA07658 standard; DNA; 20 BP.

XX AAA07658;

DT 19-JUN-2000 (first entry)

DE Forward primer for amplifying HERG gene exon 2.

KM HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; human;

KW PCR primer; ss.

OS Homo sapiens.

PM WO200006772-A1.

PD 10-FEB-2000.

PF 20-JUL-1999; 99WO-US016337.

PR 27-JUL-1998; 98US-00122847.

PR 06-JAN-1999; 99US-00226012.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

DR WPI; 2000-195319/17.

PT New isolated mutant HERG nucleic acids; useful for developing products

PT for the diagnosis, prevention and treatment of long QT syndrome.

PS Claim 7; Page 72; 163pp; English.

XX The invention relates to a HERG protein having a mutation compared to

CC wild-type HERG, and is useful for developing products for the diagnosis,

CC prevention and treatment of long QT (LQT) syndrome. The products and

CC methods can be used for the diagnosis of subjects with LQT syndrome. They

CC can also be used to screen for drugs for treating or preventing LQT

CC syndrome. The HERG nucleic acids can also be used for gene therapy and

CC HERG peptides can be used for peptide therapy. Sequences AAA07654-693

CC represent primers for amplifying HERG exons
 XX Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCCCGTCACGCGCACTCT 20
 |||||
 DB 1 GGTCCCGTCACGCGCACTCT 20

RESULT 2
 ADK60376
 ID ADK60376 standard; DNA; 29 BP.

AC ADK60376;
 DT 06-MAY-2004 (first entry)

DE Angiogenesis differentially expressed gene GS-N29 primer GV29-1.

XX ss; primer; vasotropic; antirheumatic; antiarthritic; hypotensive;
 KW antianginal; antiinflammatory; cardiac; angiogenesis inhibitor;
 KW gene therapy; angiogenesis; endothelial cell; diagnosis;
 KW tumor vascularization; retinopathy; rheumatoid arthritis;
 KW Crohn's disease; atherosclerosis; ovary hyperstimulation; psoriasis;
 KW endometriosis; restenosis; angioplasty; cicatrization;
 KW peripheral vascular disease; hypertension; vascular inflammation;
 KW Raynaud's disease; aneurism; thrombophlebitis; ischemia; angina;
 KW myocardial infarction; chronic heart disease; cardiac congestion;
 KW macular degeneration; osteoporosis.

XX Homo sapiens.

OS FR2836687-A1.

PN FR2836687-A1.

XX 05-SEP-2003.

PD 11-APR-2002; 2002FR-00004546.

XX 04-MAR-2002; 2002FR-00002717.

PR (GENE-) GENE SIGNAL.

PA (ALMA/) AL MAHMOOD S.

XX Colin S, Schneider C, Al Mahmood S;

PI WPI; 2004-013912/02.

DR Compositions for diagnosing, prognosing and treating angiogenic disorders
 XX including tumor vascularization and heart disease, comprise nucleic acid
 PT or polypeptide differentially expressed in angiogenesis.
 PS Disclosure; SEQ ID NO 252; 424bp; French.

XX The invention relates to a novel pharmaceutical composition active on
 CC angiogenesis comprising an endothelial cell nucleic acid whose expression
 CC is induced by an angiogenic factor and inhibited by an angiostatic agent
 CC or its complement or fragment, a polypeptide sequence encoded by the
 CC nucleic acid or its fragment, a molecule capable of inhibiting expression
 CC of the nucleic acid or a molecule which binds to the polypeptide
 CC sequence. The invention is used to diagnose, prognose or treat an
 CC angiogenic disorder in a mammal, particularly a human. The disorder is
 CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
 CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
 CC endometriosis associated with neovascularization, restenosis due to
 CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
 CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
 CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,
 CC myocardial infarction, chronic heart disease, cardiac congestion or
 CC macular degeneration due to age or osteoporosis. This sequence

CC corresponds to a PCR primer to amplify a differentially expressed DNA
 CC used in the composition of the invention.

XX Sequence 29 BP; 4 A; 10 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 12; Length 29;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTCCCGTCACGCGCACTCT 20
 |||||
 DB 10 GGTCCCGTCACGCGCACTCT 29

RESULT 3
 ADK60677
 ID ADK60677 standard; DNA; 29 BP.

AC ADK60677;
 DT 06-MAY-2004 (first entry)

DE Angiogenesis differentially expressed gene GS-N29 primer GV29-1.

XX ss; primer; vasotropic; antirheumatic; antiarthritic; hypotensive;
 KW antianginal; antiinflammatory; cardiac; angiogenesis inhibitor;
 KW gene therapy; angiogenesis; endothelial cell; diagnosis;
 KW tumor vascularization; retinopathy; rheumatoid arthritis;
 KW Crohn's disease; atherosclerosis; ovary hyperstimulation; psoriasis;
 KW endometriosis; restenosis; angioplasty; cicatrization;
 KW peripheral vascular disease; hypertension; vascular inflammation;
 KW Raynaud's disease; aneurism; thrombophlebitis; ischemia; angina;
 KW myocardial infarction; chronic heart disease; cardiac congestion;
 KW macular degeneration; osteoporosis.

XX Homo sapiens.

OS FR2836686-A1.

PN FR2836686-A1.

XX 05-SEP-2003.

PD 04-MAR-2002; 2002FR-00002717.

XX 04-MAR-2002; 2002FR-00002717.

PR (GENE-) GENE SIGNAL.

PA (ALMA/) AL MAHMOOD S.

XX Colin S, Schneider C, Al Mahmood S;

PI WPI; 2004-013911/02.

DR Compositions containing nucleic acid or polypeptide differentially
 XX expressed in angiogenesis are useful to diagnose, prognose and treat
 PT angiogenic disorders including tumor vascularization and heart disease.
 PS Disclosure; SEQ ID NO 252; 405bp; French.

XX The invention relates to a novel pharmaceutical composition active on
 CC angiogenesis comprising an endothelial cell nucleic acid whose expression
 CC is induced by an angiogenic factor and inhibited by an angiostatic agent
 CC or its complement or fragment, a polypeptide sequence encoded by the
 CC nucleic acid or its fragment, a molecule capable of inhibiting expression
 CC of the nucleic acid or a molecule which binds to the polypeptide
 CC sequence. The invention is used to diagnose, prognose or treat an
 CC angiogenic disorder in a mammal, particularly a human. The disorder is
 CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
 CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
 CC endometriosis associated with neovascularization, restenosis due to
 CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
 CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
 CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,
 CC myocardial infarction, chronic heart disease, cardiac congestion or

CC macular degeneration due to age or osteoporosis. This sequence
CC corresponds to a PCR primer to amplify a differentially expressed DNA
CC used in the composition of the invention.

SO Sequence 29 BP; 4 A; 10 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 12; Length 29;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGGTCACGGCACTCT 20
|||
Db 10 GGTCGGTCACGGCACTCT 29

RESULT 4

ID ADP73300 standard; DNA; 29 BP.

AC ADP73300;

DT 12-AUG-2004 (first entry)

DE Primer of vector with human antisense DNA insert, GV29-1.

KW Inhibitor; angiogenesis; antisense nucleic acid; immunisation;
KW angiogenic disorder; antiangiogenic; angiogenesis stimulator; cyclostatic;
KW dermatological; antiarthritic; antirheumatic; antiinflammatory;
KW vasotropic; hypotensive; ophthalmological; antipsoriatic; cardiac;
KW gene therapy; antisense gene therapy; tumour vascularisation;
KW retinopathies; rheumatoid arthritis; Crohn's disease; atherosclerosis;
KW ovarian hyperstimulation; psoriasis; endometriosis; restenosis;
KW tissue granulation; peripheral vascular disorder; hypertension;
KW vascular inflammation; Raynaud's disease; aneurism; arterial restenosis;
KW thrombophlebitis; lymphadenopathy; lymphedema; ischaemia; angina;
KW myocardial infarction; chronic heart disease; congestive heart disease;
KW macular degeneration; human; primer; ss.

OS Homo sapiens.
XX Unidentified.

PN FR2843753-A1.

PD 27-FEB-2004.

PF 20-JUN-2003; 2003PR-00007507.

PR 04-MAR-2002; 2002PR-00002717.

PA (GENE/) GENE S.
XX (ALMA/) AL M S.

PI Colin S, Schneider C, Al MS;

DR WPI; 2004-216677/21.

PT Antisense nucleic molecule useful as inhibitor of angiogenesis in the
PT treatment of angiogenic disorders, e.g., rheumatoid arthritis,
PT atherosclerosis and endometriosis.

PS Disclosure; SEQ ID NO 252; 404bp; French.

XX The invention relates to a novel inhibitor of angiogenesis comprising an
XX active substance chosen from at least one of a nucleic acid molecule, an
XX antisense nucleic acid molecule, a polypeptide or an antibody. The
XX invention further comprises: an antisense nucleic acid sequence chosen
XX from any of the sequences provided in the specification; preparation of
XX the antibody comprising in vivo or in vitro immunisation of an
XX immunocompetent animal cell, preferably of a vertebrate and most
XX preferably of a mammal, with at least one of the polypeptide sequences
XX chosen from a sequence provided in the specification; a mammalian
XX expression vector comprising at least one antisense sequence chosen from
XX an antisense nucleic acid provided in the specification; preparation of a

CC genetically modified cell, that over- or under-expresses a gene
CC implicated in an angiogenic disorder, comprising inserting the vector
CC from above into a mammalian cell; a genetically modified cell that over-
CC expresses or under-expresses at least one gene involved in angiogenesis
CC by a nucleic acid sequence chosen from any of ADP7049 to ADP7338, as in
CC the antisense nucleic acid selection of above, or a fragment of any of
CC these; preparation of a cell line that stably expresses an expression
CC vector. The angiogenesis inhibitor has the following activities:
CC antiangiogenic, angiogenesis stimulator, angiogenesis inhibitor,
CC cytostatic, dermatological, antarthritic, antirheumatic,
CC antiinflammatory, vasotropic, hypotensive, ophthalmological,
CC antipsoriatic, and cardiac. The novel nucleic acid molecules of the
CC invention may be used to treat disorders in gene therapy and antisense
CC gene therapy. The nucleic acid sequences, proteins and antibodies as part
CC of the therapeutic compositions are useful in treating a disorder of
CC angiogenesis chosen from: tumour vascularisation, retinopathies,
CC rheumatoid arthritis, Crohn's disease, atherosclerosis, ovarian
CC hyperstimulation, psoriasis, endometriosis associated with
CC neovascularisation, restenosis due to balloon angioplasty, tissue
CC granulation due to scarification, peripheral vascular disorders,
CC hypertension, vascular inflammation, Raynaud's disease, aneurism,
CC arterial restenosis, thrombophlebitis, lymphadenopathy, lymphedema,
CC ischaemia, angina, myocardial infarction, chronic heart disease,
CC congestive heart disease, macular degeneration linked to age and
CC osteoporosis. This polynucleotide sequence represents a primer used in
CC the exemplification of the invention.

SO Sequence 29 BP; 4 A; 10 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 12; Length 29;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGGTCACGGCACTCT 20
|||
Db 10 GGTCGGTCACGGCACTCT 29

RESULT 5

ID ADK60255/C

AC ADK60255;

DT 06-MAY-2004 (first entry)

DE Antisense DNA to angiogenesis differentially expressed GS-N29.

KW vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;
KW antiinflammatory; cardiac; angiogenesis inhibitor; gene therapy;
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
KW ischaemia; angina; myocardial infarction; chronic heart disease;
KW cardiac congestion; macular degeneration; osteoporosis; antisense; ss.

OS Homo sapiens.

PN FR2836687-A1.

PD 05-SEP-2003.

PF 11-APR-2002; 2002PR-00004546.

PA (GENE-) GENE SIGNAL.
XX (ALMA/) AL MAHMOOD S.

PI Colin S, Schneider C, Al Mahmood S;

DR WPI: 2004-013912/02.
XX Compositions for diagnosing, prognosing and treating angiogenic disorders
PT including tumor vascularization and heart disease, comprise nucleic acid
PT or polypeptide differentially expressed in angiogenesis.
XX
PS Claim 4; SEQ ID NO 131, 424pp; French.
XX
CC The invention relates to a novel pharmaceutical composition active on
CC angiogenesis comprising an endothelial cell nucleic acid whose expression
CC is induced by an angiogenic factor and inhibited by an angiostatic agent
CC or its complement or fragment, a polypeptide sequence encoded by the
CC nucleic acid or its fragment, a molecule capable of inhibiting expression
CC of the nucleic acid or a molecule which binds to the polypeptide
CC sequence. The invention is used to diagnose, prognose or treat an
CC angiogenic disorder in a mammal, particularly a human. The disorder is
CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
CC endometriosis associated with neovascularization, restenosis due to
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,
CC myocardial infarction, chronic heart disease, cardiac congestion or
CC macular degeneration due to age or osteoporosis. This sequence
CC corresponds to an antisense DNA sequence to a differentially expressed
CC DNA used in the composition of the invention.
XX
SQ Sequence 564 BP; 138 A; 164 C; 118 G; 144 T; 0 U; 0 Other;
XX
Query Match 84.0%; Score 16.8; DB 12; Length 564;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GGTCCGTCACGCGCACTCT 20
|||
Db 564 GGTCCGTCACGCGCACTCT 545
XX
RESULT 6
ADK60556/c
ID ADK60556 standard; DNA; 564 BP.
XX
AC ADK60556;
XX
DT 06-MAY-2004 (first entry)
XX
DE Antisense DNA to angiogenesis differentially expressed GS-N29.
XX
KW vasoactive; antithrombotic; antithrombotic; hypotensive; antianginal;
KW antiinflammatory; cardiac; angiogenesis inhibitor; gene therapy;
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
KW ischemia; angina; myocardial infarction; chronic heart disease;
KW cardiac congestion; macular degeneration; osteoporosis; antisense; ss.
XX
OS Homo sapiens.
XX
PN FR2836686-A1.
XX
PD 05-SEP-2003.
XX
PF 04-MAR-2002; 2002FR-00002717.
XX
PR 04-MAR-2002; 2002FR-00002717.
XX
PA (GENE-) GENE SIGNAL.
XX (ALMA/) AL MAHMOOD S.
XX
PI Colin S, Schneider C, Al Mahmood S;
XX

DR WPI: 2004-013911/02.
XX Compositions containing nucleic acid or polypeptide differentially
PT expressed in angiogenesis are useful to diagnose, prognose and treat
PT angiogenic disorders including tumor vascularization and heart disease.
XX
PS Claim 4; SEQ ID NO 131, 405pp; French.
XX
CC The invention relates to a novel pharmaceutical composition active on
CC angiogenesis comprising an endothelial cell nucleic acid whose expression
CC is induced by an angiogenic factor and inhibited by an angiostatic agent
CC or its complement or fragment, a polypeptide sequence encoded by the
CC nucleic acid or its fragment, a molecule capable of inhibiting expression
CC of the nucleic acid or a molecule which binds to the polypeptide
CC sequence. The invention is used to diagnose, prognose or treat an
CC angiogenic disorder in a mammal, particularly a human. The disorder is
CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
CC endometriosis associated with neovascularization, restenosis due to
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,
CC myocardial infarction, chronic heart disease, cardiac congestion or
CC macular degeneration due to age or osteoporosis. This sequence
CC corresponds to an antisense DNA sequence to a differentially expressed
CC DNA used in the composition of the invention.
XX
SQ Sequence 564 BP; 138 A; 164 C; 118 G; 144 T; 0 U; 0 Other;
XX
Query Match 84.0%; Score 16.8; DB 12; Length 564;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GGTCCGTCACGCGCACTCT 20
|||
Db 564 GGTCCGTCACGCGCACTCT 545
XX
RESULT 7
ADP73179/c
ID ADP73179 standard; DNA; 564 BP.
XX
AC ADP73179;
XX
DT 12-AUG-2004 (first entry)
XX
DE Angiogenesis inhibitor human DNA antisense region of GS-N29 and GS-N52.
XX
KW inhibitor; angiogenesis; antisense nucleic acid; immunization;
KW angiogenic disorder; antiangiogenic; angiogenesis stimulator; cytostatic;
KW dermatological; antithrombotic; antithrombotic; antiinflammatory;
KW vasoactive; hypotensive; ophtalmological; antipsoriatic; cardiac;
KW gene therapy; antisense gene therapy; tumor vascularization;
KW retinopathies; rheumatoid arthritis; Crohn's disease; atherosclerosis;
KW ovarian hyperstimulation; psoriasis; endometriosis; restenosis;
KW tissue granulation; peripheral vascular disorder; hypertension;
KW vascular inflammation; Raynaud's disease; aneurism; arterial restenosis;
KW thrombophlebitis; lymphedema; lymphedema; ischemia; angina;
KW myocardial infarction; chronic heart disease; congestive heart disease;
KW macular degeneration; human; ss.
XX
OS Homo sapiens.
XX
PN FR2843753-A1.
XX
PD 27-FEB-2004.
XX
PF 20-JUN-2003; 2003FR-00007507.
XX
PR 04-MAR-2002; 2002FR-00002717.
XX
PA (GENE/) GENE S.
XX (ALMS/) AL M S.
XX

PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423113P.
PR 05-NOV-2002; 2002US-0042378P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alabrook JP, Alvarez E, Anderson DM, Boldog FL, Casman SJ,
XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K,
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X,
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR,
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS,
PI Padigaru M, Patturajan M, Pena CE, Reymen JA, Raha D, Rastelli L,
PI Rieger DK, Rotenberg ME, Sciore P, Shenoy SG, Shinkets RA,
PI Smlthson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M,
XX Zhong H;
XX WPI: 2004-081935/08.
DR P-PSDB: ADH72104.
XX
XX New NOXV polypeptides and nucleic acid molecules useful for preventing or
PT treating NOXV-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 43; SEQ ID NO 999; 1880bp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOXV). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOXV polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOXV-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOXV polypeptide of the invention.
XX
SQ Sequence 2136 BP; 591 A; 471 C; 550 G; 524 T; 0 U; 0 Other;
Query Match 84.0%; Score 16.8; DB 12; Length 2136;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTCCCGTCAGCGCACTCT 20
DB 1259 GGTCCCGTCAGCGCACTCT 1278
RESULT 9
ACAI0119
ID ACAI0119 standard; cDNA, 2153 BP.
XX
XX ACAI0119;
XX
XX 02-JUN-2003 (first entry)
XX
XX Human NOXV polynucleotide #9.
XX

KW Human, NOXV; gene; ss; metabolic disorder; diabetes; infectious disease;
KW obesity; anorexia; cancer; cardiovascular disorder; asthma; neurogenesis;
KW neurodegenerative disorder; epilepsy; immune disorder; osteoarthritis;
KW haematopoietic disorder; inflammatory skin disorder; dyslipidemia;
KW haematopoiesis; wound healing; angiogenesis; bacterial infection;
KW viral infection; fungal infection; helminthic infection; atherosclerosis;
KW protozoal infection; hypertension.
XX
XX Homo sapiens.
OS
XX MO200290504-A2.
XX
XX 14-NOV-2002.
XX
XX
XX 02-MAY-2002; 2002WO-US014342.
XX
XX
XX 03-MAY-2001; 2001US-0288395P.
PR 04-MAY-2001; 2001US-0288900P.
PR 07-MAY-2001; 2001US-0289087P.
PR 14-MAY-2001; 2001US-0290753P.
PR 15-MAY-2001; 2001US-0291189P.
PR 16-MAY-2001; 2001US-0291243P.
PR 18-MAY-2001; 2001US-0292001P.
PR 21-MAY-2001; 2001US-0292374P.
PR 22-MAY-2001; 2001US-0292587P.
PR 23-MAY-2001; 2001US-0293107P.
PR 29-MAY-2001; 2001US-0294110P.
PR 30-MAY-2001; 2001US-0294434P.
PR 31-MAY-2001; 2001US-0294827P.
PR 18-JUN-2001; 2001US-0298988P.
PR 31-JUL-2001; 2001US-0308901P.
PR 17-AUG-2001; 2001US-0313388P.
PR 21-AUG-2001; 2001US-0313851P.
PR 21-AUG-2001; 2001US-0313937P.
PR 17-SEP-2001; 2001US-0322701P.
PR 17-SEP-2001; 2001US-0322802P.
PR 25-SEP-2001; 2001US-0324757P.
PR 27-SEP-2001; 2001US-0325314P.
PR 27-SEP-2001; 2001US-0325682P.
PR 21-NOV-2001; 2001US-0332129P.
PR 03-DEC-2001; 2001US-0336882P.
PR 14-DEC-2001; 2001US-0340305P.
PR 01-MAY-2002; 2002US-00138588.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alabrook JP, Anderson DM, Boldog FL, Burgess CE, Casman SJ;
PI Chapoval A, Edinger S, Gerlach V, Gorman L, Gunther E, Guo X;
PI Kekuda R, Lepley DM, Li L, Liu X, Malyankar UM, Miller CE,
PI Millet I, Padigaru M, Patturajan M, Pena CE, Rieger DK, Shenoy SG,
PI Shinkets RA, Spytek KA, Taupier RJ, Vernet CAM, Voss EZ,
PI Zerhusen BD;
XX
XX WPI: 2003-103512/09.
DR P-PSDB: ABU69134.
XX
XX New isolated NOXV polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOXV-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX
XX Claim 20; Page 100-101; 340pp; English.
XX
XX The invention relates to human NOXV polypeptides and the polynucleotides
XX encoding them. The polypeptides, polynucleotides and antibodies that bind
XX immunospecifically to the polypeptides are useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease,
XX preferably a NOXV-associated disorder. The sequences are useful for
XX treating, preventing or diagnosing diseases such as metabolic disorders,
XX diabetes, obesity, infectious diseases (viral, bacterial, fungal,
XX helminthic, and protozoal), anorexia, cancer, cardiovascular disorders
XX (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g.
XX Alzheimer's disease, Parkinson's disease), epilepsy, immune disorders,
XX

RESULT 12
ADGC30192
ID ADGC30192 standard; cDNA; 2517 BP.
XX
XX
ADGC30192;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA sequence, SEQ ID NO:274.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; ancaemic; anticoagulant; thrombolytic; vulnery;
KW anticancer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Tang Y, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX
DR WPI: 2003-371981/35.
XX
DR P-PSDB; ADGC31163.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
PT
Claim 1; SEQ ID NO 274; 1185bp; English.
XX
PS The invention relates to 971 novel human cDNA sequences (ADGC29919-
XX ADGC30889) and the polypeptides thereof (ADGC30890-ADGC3160). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADGC31601-ADGC32627) and the polypeptides encoded by the contigs (ADGC2628
CC -ADGC3394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC

```

CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX Sequence 2517 BP; 755 A; 496 C; 570 G; 696 T; 0 U; 0 Other;
SQ
Query Match      84.0%; Score 16.8; DB 10; Length 2517;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1 GGTCCGTCAGCGGCACTCT 20
      ||||| ||||| ||||| |||||
DB      527 GGTCTGTGTCAGCGGCACTCT 546
RESULT 13
ADL63644
ID      ADL63644 standard; DNA; 3407 BP.
XX
XX      ADL63644;
XX
DT      20-MAY-2004 (first entry)
DB      Human ovarian cancer DNA marker #21856.
XX
XX      Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX      Homo sapiens.
XX
XX      WO200170979-A2.
XX
XX      27-SEP-2001.
XX
XX      21-MAR-2001; 2001WO-US009126.
XX
XX      21-MAR-2000; 2000US-0191031P.
XX      25-MAY-2000; 2000US-0207124P.
XX      15-JUN-2000; 2000US-0211940P.
XX      07-JUL-2000; 2000US-0216820P.
XX      25-JUL-2000; 2000US-0220661P.
XX      21-DEC-2000; 2000US-0257672P.
XX
XX      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX      Lee J, Little J;
XX
XX      WPI; 2001-611502/70.
XX
XX      Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX      cancer cells as compared to their normal non-cancerous ovarian cells are
XX      used to characterize stage, grade, histological type of ovarian cancer.
XX
XX      Disclosure; SEQ ID NO 21856; 106pp; English.
XX
XX      The invention relates to nucleic acid markers which are overexpressed in
XX      ovarian cancer cells as compared to their expression in normal (i.e. non-
XX      cancerous) ovarian cells. The invention also relates to polypeptides
XX      encoded by the markers, antibodies that selectively bind to the
XX      polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX      of developing ovarian cancer involving inhibiting expression of a gene
XX      corresponding to a marker of the invention and a method of treating a
XX      patient afflicted with ovarian cancer comprising providing to cells of
XX      the patient an antisense oligonucleotide complementary to a marker of the
XX      invention. The markers are useful for assessing if a patient is afflicted
XX      with ovarian cancer, which involves comparing the level of expression of
XX      a marker in a patient sample and a normal level of expression of the
XX      marker in a control non-ovarian cancer sample. A difference between the
XX      expression levels indicates ovarian cancer. The level of expression of a
XX      marker corresponds to a secreted protein or to a transcribed
XX      polynucleotide or its portion. The level of expression of the marker is

```

CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX
SQ Sequence 3407 BP; 1032 A; 646 C; 687 G; 1035 T; 0 U; 7 Other;

Query Match 84.0%; Score 16.8; DB 5; Length 3407;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCCCGTCAGCGCACTCT 20
Db 310 GGTCCCTGTACGCGCACTCT 329

RESULT 14
AA68120
ID AA68120 standard; cDNA, 3910 BP.
XX
AC AA68120;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #3924.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG03933.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX
PS Claim 1; SEQ ID NO 3924; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probe, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (I) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA64197-AA694564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_ptc_sequences

XX
SQ Sequence 3910 BP; 1098 A; 875 C; 998 G; 939 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 5; Length 3910;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCCCGTCAGCGCACTCT 20
Db 2573 GGTCCCGTCAGGCGCACTCT 2592

RESULT 15
AA172024
ID AA172024 standard; cDNA, 4073 BP.
XX
AC AA172024;
XX
DT 04-MAR-2002 (first entry)
XX
DE Human thrombospondin protein, BT.012, coding sequence.
XX
KW Human; thrombospondin; BT.012; thrombospondin repeat domain; modulation;
KW angiogenesis; cancer; metastasis; diabetic retinopathy;
KW macular degeneration; cardiovascular disease; wound; ss.
XX
OS Homo sapiens.
XX
FN Key Location/Qualifiers
FN CDS 1..4011
FT /*tag= a
FT /product= "BT.012"
FT /transl_except= {pos:3973..3975, aa:Glu}

XX
PN WO200174852-A2.
XX
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US010222.
XX
PR 31-MAR-2000; 2000US-0266300P.
XX
PA (FARB) BAYER CORP.
XX
PI Chen J, Chen D, Zolotorov A, Davies CJ, Wetzel GD;
PI Dubois-Stringfellow NA;
XX
DR WPI; 2002-066297/09.
DR P-PSDB; AAB47771.
XX
PT Novel protein designated BT.012 has a thrombospondin repeat and inhibits
PT angiogenesis, and is useful to treat cancer, diabetic retinopathy,
PT macular degeneration, cardiovascular disease and wounds.

XX
PS Claim 15; Page 53-54; 54pp; English.

XX
CC This sequence encodes a human thrombospondin protein, BT.012. A fragment
CC of this protein, comprising a thrombospondin repeat domain, may be used
CC to modulate angiogenesis at a site. The BT.012 fragment may be used for
CC diagnosing, preventing or treating a medical condition, particularly

CC cancer, metastasis, diabetic retinopathy, macular degeneration,
CC cardiovascular disease or a wound
XX
SQ Sequence 4073 BP; 1111 A; 934 C; 1020 G; 1008 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 6; Length 4073;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GATCCCGTCACGCGCACTCT 20
|||
Db 1799 GATCCCGTCACGCGCACTCT 1818

Search completed: April 10, 2006, 15:24:12
Job time : 222.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2006, 14:56:10 ; Search time 1128.5 Seconds
(without alignments)
1007.416 Million cell updates/sec

Title: US-10-696-708a-60

Perfect score: 20

Sequence: 1 GGTCCGTCACGCGCACTCT 20

Scoring table: IDENTITY NUC

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sci:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR139543 Sequence
2	20	100.0	20	6	BD223632 Mutations
3	20	100.0	20	6	CS124258 Sequence
4	17	85.0	4185	15	AP006387 Lotus cor
5	17	85.0	79136	14	AP007610 Lotus cor
6	17	85.0	80930	15	AP004894 Lotus cor
7	17	85.0	82389	15	AP004909 Lotus cor
8	17	85.0	91117	14	AP007711 Lotus cor
9	17	85.0	94745	15	AP006653 Lotus cor
10	17	85.0	104684	15	AP006124 Lotus cor
11	17	85.0	104729	15	AP006082 Lotus cor
12	17	85.0	108554	14	AP008010 Lotus cor
13	17	85.0	113103	14	AP007977 Lotus cor
14	16.8	84.0	29	6	AX828606 Sequence
15	16.8	84.0	564	6	AX828485 Sequence
16	16.8	84.0	691	6	AF403188 Unculture
17	16.8	84.0	694	3	AY100534 Unculture
18	16.8	84.0	1045	2	AY427449 Flabellin

RESULT 1	AR139543	20 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR139543	Sequence 60 from patent US 6207383.			
DEFINITION	AR139543				
ACCESSION	AR139543.1	GI:14482039			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Keating,M.T. and Splawski,I.				
JOURNAL	Mutations in and genomic structure of HERG--a long QT syndrome gene				
FEATURES	Patent: US 6207383-A 60 27-MAR-2001;				
source	Location/Qualifiers				
	1..20				
	/organism="unknown"				
	/mol_type="unassigned DNA"				

ALIGNMENTS

Query Match	100.0%	Score 20;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches	20;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
QY	1	GGTCCGTCACGCGCACTCT 20		
Db	1	GGTCCGTCACGCGCACTCT 20		
RESULT 2				
LOCUS	BD223632	20 bp	DNA	linear
DEFINITION	BD223632	Mutations in and genomic structure of HERG - a long QT syndrome gene.		
ACCESSION	BD223632	GI:33033402		
VERSION	BD223632.1	JP 200521065-A/58.		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			

REFERENCE 1 (bases 1 to 20)
 AUTHORS Keating, M.T. and Splawski, I.
 TITLE Mutations in and genomic structure of HERG - a long QT syndrome gene
 JOURNAL Patent: JP 2002521065-A 58 16-JUL-2002;
 COMMENT UNIVERSITY OF UTAH RESEARCH FOUNDATION
 OS Homo sapiens (human)
 PN JP 2002521065-A/58
 PD 16-JUL-2002
 PF 20-JUL-1999 JP 2000562554
 PR 27-JUL-1998 US 09/122847,06-JAN-1999 US 09/226012 PI
 PC MARK T KEATING, IGOR SPLAWSKI
 PC C12N15/09, A01K67/027, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
 C12N1/21, PC
 C12N5/10, C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/566, G01N33/577//C12P21/08, C12N15/00, C12N5/00, PC
 C12N5/00, CC
 CC Mutations in and genomic structure of HERG - a long QT CC
 FH syndrome gene Location/Qualifiers
 FT source 1..20
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCGTCACGCGCACTCT 20
 1 GGTCCGTCACGCGCACTCT 20

Db 1 GGTCCGTCACGCGCACTCT 20

RESULT 3
 CS124258 20 bp DNA linear PAT 21-JUL-2005
 LOCUS Sequence 60 from Patent EP1553190.
 DEFINITION CS124258
 ACCESSION CS124258
 VERSION CS124258.1 GI:71057341
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catearrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Keating, M.T.
 TITLE Mutations in and genomic structure of HERG - a long QT syndrome gene
 JOURNAL Patent: EP 1553190-A 60 13-JUL-2005;
 COMMENT The University of Utah Research Foundation (US)
 FEATURES
 source Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCGTCACGCGCACTCT 20
 1 GGTCCGTCACGCGCACTCT 20

Db 1 GGTCCGTCACGCGCACTCT 20

RESULT 4
 AP006387/c 4185 bp DNA linear PLN 22-JUL-2003
 LOCUS Lotus corniculatus var. japonicus genomic DNA, chromosome 1,
 DEFINITION clone:UJT9K18, TM0252c, complete sequence.
 ACCESSION AP006387
 VERSION AP006387.1 GI:31581018
 KEYWORDS HTG.
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
 ORGANISM Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

REFERENCE 1
 AUTHORS Asamizu, E., Kato, T., Sato, S., Nakamura, Y., Kaneko, T. and Tabata, S.
 TITLE Structural Analysis of a Lotus japonicus Genome. IV. Sequence Features and Mapping of seventy-three TAC clones which cover the 7.5 Mb Regions of the Genome
 JOURNAL DNA Res. (2003) In press
 REFERENCE 2 (bases 1 to 4185)
 AUTHORS Sato, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan [E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/, Tel: 81-438-52-3935 (ex. 2337), Fax: 81-438-52-3934]
 FEATURES
 source Location/Qualifiers
 1..4185
 /organism="Lotus corniculatus var. japonicus"
 /mol_type="genomic DNA"
 /variety="japonicus"
 /db_xref="taxon:34305"
 /chromosome="1"
 /clone="UJT9K18"
 /clone_1ib="UJT library"
 /note="TM0252c, a part of TAC clone: TM0252.
 synonym: Lotus japonicus"

ORIGIN
 Query Match 85.0%; Score 17; DB 15; Length 4185;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCCCGTCACGCGCACTC 19
 1 TCCCGTCACGCGCACTC 19

Db 1191 TCCCGTCACGCGCACTC 1175

RESULT 5
 AP007610 79136 bp DNA linear HTG 28-DEC-2004
 LOCUS Lotus corniculatus var. japonicus clone UJT11B21, *** SEQUENCING IN
 DEFINITION PROGRESS ***; 21 unordered pieces.
 ACCESSION AP007610
 VERSION AP007610.1 GI:56805923
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
 ORGANISM Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

REFERENCE 1
 AUTHORS Kaneko, T., Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE Structural Analysis of a Lotus japonicus Genome. XI. Sequence Features and Mapping of Nine hundred twenty-one TAC Clones
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 79136)
 AUTHORS Sato, S.

TITLE
JOURNAL

Direct Submission
Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu,
Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(fax.2337),
Fax:81-438-52-3934)

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2478: contig of 2478 bp in length
2479 2578: gap of unknown length
2579 3793: contig of 1215 bp in length
3794 3893: gap of unknown length
3894 4657: contig of 764 bp in length
4658 4757: gap of unknown length
4758 5709: contig of 952 bp in length
5710 5809: gap of unknown length
5810 6112: contig of 303 bp in length
6113 6212: gap of unknown length
6213 7577: contig of 1365 bp in length
7578 7677: gap of unknown length
7678 8888: contig of 1211 bp in length
8889 8988: gap of unknown length
8989 10432: contig of 1444 bp in length
10433 10532: gap of unknown length
10533 12734: contig of 2202 bp in length
12735 12834: gap of unknown length
12835 14557: contig of 1723 bp in length
14558 14657: gap of unknown length
14658 16002: contig of 1345 bp in length
16003 16102: gap of unknown length
16103 18348: contig of 2246 bp in length
18349 18448: gap of unknown length
18449 22509: contig of 4061 bp in length
22510 22609: gap of unknown length
22610 25097: contig of 2488 bp in length
25098 25197: gap of unknown length
25198 30149: contig of 4952 bp in length
30150 30249: gap of unknown length
30250 34950: contig of 4701 bp in length
34951 35050: gap of unknown length
35051 40867: contig of 5817 bp in length
40868 40967: gap of unknown length
40968 47770: contig of 6803 bp in length
47771 47870: gap of unknown length
47871 54765: contig of 6895 bp in length
54766 54865: gap of unknown length
54866 75900: contig of 21035 bp in length
75901 76000: gap of unknown length
76001 79136: contig of 3136 bp in length.

FEATURES

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/variety="japonicus"
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/clone_lib="J1T11B21"
/note="TAC clone: TM0814, synonym: Lotus japonicus"
2479..2578
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3794..3893
/estimated_length=unknown
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5710..5809
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6113..6212

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred.No.16e+03; DB 14; Length 79136;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCCCGTCACGCGCCTC 19
|||||
Db 20335 TCCCGTCACGCGCCTC 20351

RESULT 6

AP004894/c

Lotus corniculatus var. japonicus genomic DNA, chromosome 5,
LOCUS clone:J1T17D01, TM0024, complete sequence.

DEFINITION

AP004894

ACCESSION

AP004894

VERSION

AP004894.1

KEYWORDS

HTG.

SOURCE

Lotus corniculatus var. japonicus (Lotus japonicus)

ORGANISM

Lotus corniculatus var. japonicus

REFERENCE

1

AUTHORS

Kaneko, T., Nakamura, Y., Asamizu, E., Kato, T., Sato, S. and Tabata, S.

TITLE

Structural Analysis of a Lotus japonicus Genome. I. Sequence

JOURNAL

Features and Mapping of Sixty-six TAC clones which cover the 6.7 Mb

REFERENCE

Unpublished

2 (bases 1 to 80930)

Nakamura, Y.

JOURNAL

Direct Submission

Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Research

Institute, Department of Plant Gene Research; 1532-3, Yana,

Kisarazu, Chiba 292-0812, Japan (E-mail:yn@kazusa.or.jp,
URL:http://www.kazusa.or.jp, Tel:81-438-52-3935,
Fax:81-438-52-3934)

FEATURES

Location/Qualifiers

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/clone="LJT25F20"
/clone_lib="LJT library"
/notes="TAC clone:TW0967, synonym:Lotus japonicus"
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ORIGIN

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Db      80574 TCCCGTCACGCGCCTC 80590

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RESULT 9
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LOCUS Lotus corniculatus var. japonicus genomic DNA, chromosome 2,
DEFINITION clone:LJT05M24, TW0338, complete sequence.
ACCESSION AP006653
VERSION AP006653.1 GI:41688338
XREFS HTG.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
REFERENCE 1
AUTHORS Kato,T., Sato,S., Nakamura,Y., Kaneko,T., Asamizu,E. and Tabata,S.
TITLE Structural Analysis of a Lotus japonicus Genome. V. Sequence
Features and Mapping of Sixty-four TAC Clones Which Cover the 6.4
Mb Regions of the Genome
JOURNAL DNA Res. 10, 277-285 (2003)
REFERENCE 2
AUTHORS Sato,S.

```

```

TITLE Direct Submission
JOURNAL Submitted (12-NOV-2003) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu,
Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Fax:81-438-52-3934)

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FEATURES

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source Location/Qualifiers
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/clone_lib="LJT library"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1938 TCCCGTCACGCGCCTC 1954

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RESULT 10
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LOCUS Lotus corniculatus var. japonicus genomic DNA, chromosome 3,
DEFINITION clone:LJT15N01, TW0209, complete sequence.
ACCESSION AP006124
VERSION AP006124.1 GI:29122763
XREFS HTG.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
REFERENCE 1
AUTHORS Kaneko,T., Asamizu,E., Kato,T., Sato,S., Nakamura,Y. and Tabata,S.
TITLE Structural analysis of a Lotus japonicus genome. III. Sequence
features and mapping of sixty-two TAC clones which cover the 6.7 Mb
regions of the genome
JOURNAL DNA Res. 10 (1), 27-33 (2003)
PUBMED 12693552
REFERENCE 2 (bases 1 to 104684)
AUTHORS Sato,S.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu,
Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Fax:81-438-52-3934)

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FEATURES

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source Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3 TCCCGTCACGCGCACTC 19
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 Db 49756 TCCCGTCACGCGCACTC 49740

RESULT 11
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 LOCUS Lotus corniculatus var. japonicus genomic DNA, chromosome 4,
 DEFINITION clone:UJT1E04, TW0126, complete sequence.
 ACCESSION AP006082
 VERSION AP006082.1 GI:29122721
 KEYWORDS HTG.
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
 ORGANISM Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
 Lotus.

REFERENCE
 AUTHORS Kaneko, T., Asamizu, E., Kato, T., Sato, S., Nakamura, Y. and Tabata, S.
 TITLE Structural analysis of a Lotus japonicus genome. III. Sequence
 features and mapping of sixty-two TAC clones which cover the 6.7 Mb
 regions of the genome
 JOURNAL DNA Res. 10 (1), 27-33 (2003)
 PUBMED 12693552
 REFERENCE 2 (bases 1 to 104729)
 AUTHORS Sato, S.
 TITLE Direct Submission
 JOURNAL Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute,
 Department of Plant Gene Research, 2-6-7 Kazusa-Kamatari, Kisarazu,
 Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
 URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
 Fax:81-438-52-3934)

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 Best Local Similarity 100.0%; Pred.No.1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TCCCGTCACGCGCACTC 19
 |||||
 Db 89978 TCCCGTCACGCGCACTC 89962

RESULT 12
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 LOCUS Lotus corniculatus var. japonicus chromosome 1 clone UJT1C12. ***
 DEFINITION SEQUENCING IN PROGRESS ***, 31 unordered pieces.
 ACCESSION AP008010
 VERSION AP008010.1 GI:56806318
 KEYWORDS HTG; HTGS PHASE1.
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
 ORGANISM Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
 Lotus.

REFERENCE
 AUTHORS Kaneko, T., Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE Structural Analysis of a Lotus japonicus Genome. XI. Sequence

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Features and Mapping of Nine hundreded twenty-one TAC Clones
 Unpublished
 2 (bases 1 to 108554)
 Sato, S.
 Direct Submission
 Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,
 Department of Plant Gene Research, 2-6-7 Kazusa-Kamatari, Kisarazu,
 Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
 URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
 Fax:81-438-52-3934)
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 31 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 1100 1199: gap of unknown length
 1200 1865: contig of 666 bp in length
 1866 1965: gap of unknown length
 1966 3059: contig of 1094 bp in length
 3060 3159: gap of unknown length
 3160 4047: contig of 888 bp in length
 4048 4147: gap of unknown length
 4148 5292: contig of 1145 bp in length
 5293 5392: gap of unknown length
 5393 7060: contig of 1668 bp in length
 7061 7160: gap of unknown length
 7161 8524: contig of 1364 bp in length
 8525 8624: gap of unknown length
 8625 10181: contig of 1557 bp in length
 10182 10281: gap of unknown length
 10282 12241: contig of 1960 bp in length
 12242 12341: gap of unknown length
 12342 13383: contig of 1642 bp in length
 13383 14083: gap of unknown length
 14083 16429: contig of 2346 bp in length
 16430 16529: gap of unknown length
 16530 19594: contig of 3065 bp in length
 19595 19694: gap of unknown length
 19695 21638: contig of 1944 bp in length
 21639 21738: gap of unknown length
 21739 23783: contig of 2045 bp in length
 23784 23883: gap of unknown length
 23884 26140: contig of 2257 bp in length
 26141 26240: gap of unknown length
 26241 28548: contig of 2308 bp in length
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 32431 32530: gap of unknown length
 32531 35928: contig of 3398 bp in length
 35929 36028: gap of unknown length
 36029 39458: contig of 3430 bp in length
 39459 39558: gap of unknown length
 39559 42773: contig of 3215 bp in length
 42774 42873: gap of unknown length
 42874 45586: contig of 2713 bp in length
 45587 45686: gap of unknown length
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 49271 49370: gap of unknown length
 49371 54310: contig of 4940 bp in length
 54311 54410: gap of unknown length
 54411 59051: contig of 4641 bp in length
 59052 59151: gap of unknown length
 59152 64976: contig of 5825 bp in length
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 65077 69983: contig of 4907 bp in length
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 70084 74749: contig of 4666 bp in length
 74750 74849: gap of unknown length
 74850 82329: contig of 7480 bp in length


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FEATURES
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* 82430 91676: contig of 9247 bp in length
* 91677 91776: gap of unknown length
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/notes="TAC clone: TM1347, synonym: Lotus japonicus"
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 26448 TCCCGTCACGCGCACTC 26464
Qy 3 TCCCGTCACGCGCACTC 19
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DEFINITION Lotus corniculatus var. japonicus chromosome 1 clone LJT11C02, ***
ACCESSION AP007977
VERSION AP007977.1 GI:56806285
KEYWORDS HTG; HTGS PHASE1.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
REFERENCE 1
AUTHORS Kaneo, T., Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE Structural Analysis of a Lotus japonicus Genome. XI. Sequence
Features and Mapping of Nine hundred twenty-one TAC Clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 113103)
AUTHORS Sato, S.
TITLE Direct Submision
JOURNAL Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research, 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba, 292-0818, Japan (E-mail: ssato@kazusa.or.jp,
URL: http://www.kazusa.or.jp/, Tel: 81-438-52-3935 (ex. 2337),
Fax: 81-438-52-3934)
COMMENT
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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2323: contig of 1477 bp in length
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3899: gap of unknown length
3900: contig of 1011 bp in length
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5011: contig of 1107 bp in length
6118: gap of unknown length
6217: gap of unknown length
8118: contig of 1901 bp in length
8218: gap of unknown length
8219: gap of unknown length
9955: contig of 1737 bp in length
10056: gap of unknown length
12353: contig of 2298 bp in length
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15098: contig of 2645 bp in length
15198: gap of unknown length
15199: gap of unknown length
17372: contig of 2174 bp in length
17472: gap of unknown length
21212: contig of 3740 bp in length
21312: gap of unknown length
21313: gap of unknown length
24814: contig of 3502 bp in length
24914: gap of unknown length
24915: gap of unknown length
28377: contig of 3463 bp in length
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* 28478 33236: contig of 4759 bp in length
* 33237 33336: gap of unknown length
* 33337 39155: contig of 5819 bp in length
* 39155 39255: gap of unknown length
* 39255 45778: contig of 6523 bp in length
* 45778 45879: gap of unknown length
* 45879 52210: contig of 6332 bp in length
* 52210 52311: gap of unknown length
* 52311 60830: contig of 8520 bp in length
* 60830 60931: gap of unknown length
* 60931 69310: contig of 8380 bp in length
* 69310 69410: gap of unknown length
* 69410 78732: contig of 9322 bp in length
* 78732 78832: gap of unknown length
* 78832 96728: contig of 17896 bp in length
* 96728 96829: gap of unknown length
* 96829 113103: contig of 16275 bp in length.
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/variety="japonicus"
/db_xref="taxon:34305"
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TCCCGTCACGCGCACTC 19
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Db 24656 TCCCGTCACGCGCACTC 24640

RESULT 14
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LOCUS Sequence 252 from Patent WO03074073. 29 bp DNA linear PAT 12-DEC-2003
DEFINITION AX828606
ACCESSION AX828606
VERSION AX828606.1 GI:39838557
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1
Al-Mahmood, S., Colin, S. and Schneider, C.
Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
Patent: WO 03074073-A 252 12-SEP-2003;
Gene Signal (FR)
Location/Qualifiers
1. 29
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Best Local Similarity 90.0%; Pred. No. 4.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTCCGTCACGCGCACTCT 20
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Db 10 GGTCCGTCACGCGCACTCT 29

RESULT 15
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DEFINITION Sequence 131 from Patent WO03074073.
ACCESSION AX828485
VERSION AX828485.1 GI:39838436
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1
Al-Mahmood, S., Colin, S. and Schneider, C.
Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
Patent: WO 03074073-A 131 12-SEP-2003;
Gene Signal (FR)
Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTCCGTCACGCGCACTCT 20
|||||
Db 564 GGTCCGTCACGCGCACTCT 545

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Search completed: April 10, 2006, 16:19:48
Job time : 1133.5 secs

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